CAP 5510: Introduction to Bioinformatics
CGS 5166: Bioinformatics Tools

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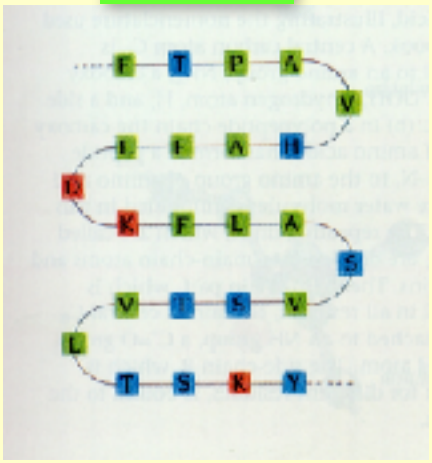
www.cis.fiu.edu/~giri/teach/BioinfF18.html

Proteins and Protein Structure

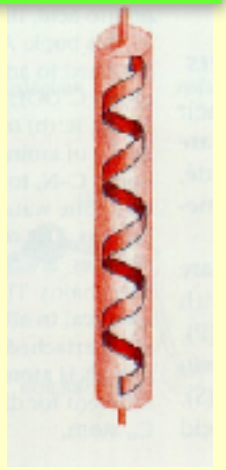
Protein Structures

- Sequences of amino acid residues
- 20 different amino acids

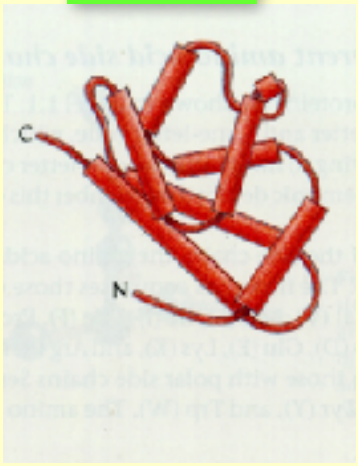
Primary



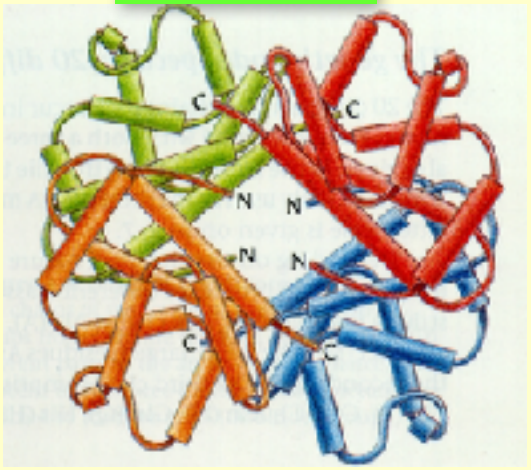
Secondary



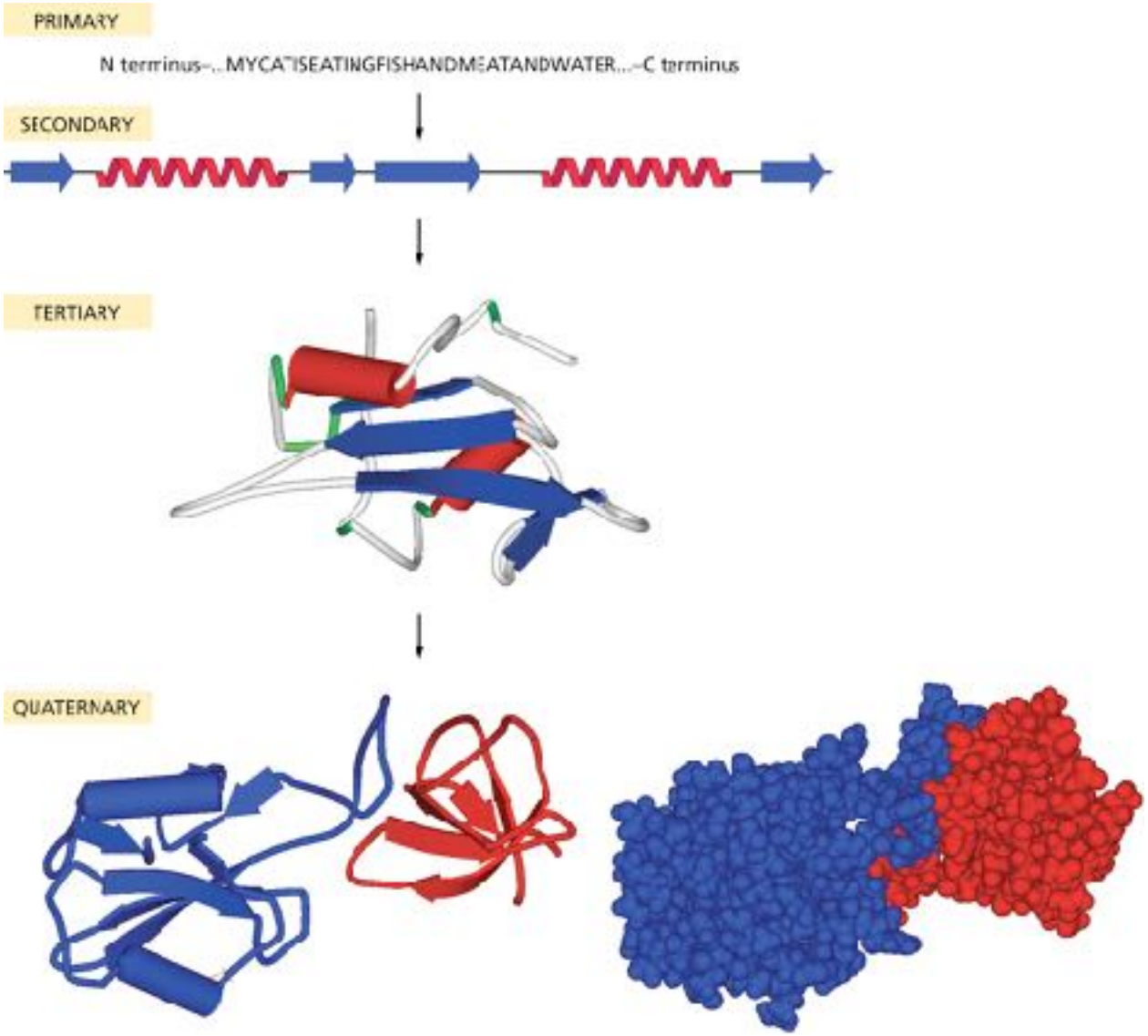
Tertiary



Quaternary



Proteins: Levels of Description



Proteins

- **Primary structure** is the sequence of amino acid residues of the protein, e.g., Flavodoxin:

  AKIGLFYGTQTGVTQTIAESIQQEFGGESIVDLNDIANADA…

- Different regions of the sequence form local regular **secondary structures**, such as Alpha helix, beta strands, etc.

  AKIGLFYGTQTGVTQTIAESIQQEFGGESIVDLNDIANADA…

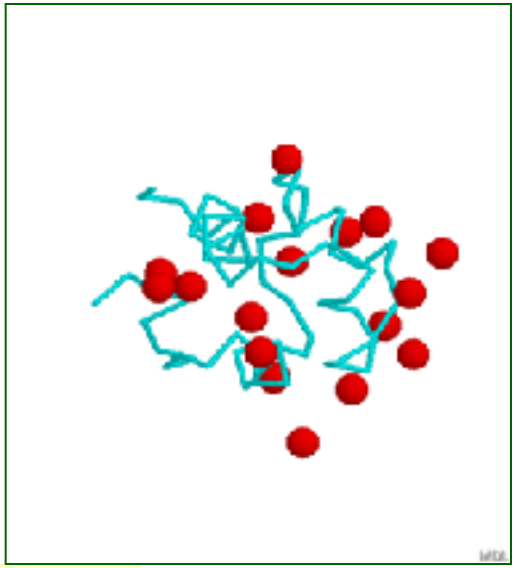
More on Secondary Structures

- **α-helix**
  - Main chain with peptide bonds
  - Side chains project outward from helix
  - Stability provided by H-bonds between CO and NH groups of residues 4 locations away.
- **β-strand**
  - Stability provided by H-bonds with one or more β-strands, forming β-sheets. Needs a β-turn.

Proteins

- **Tertiary structures** are formed by packing secondary structural elements into a globular structure.

Myoglobin

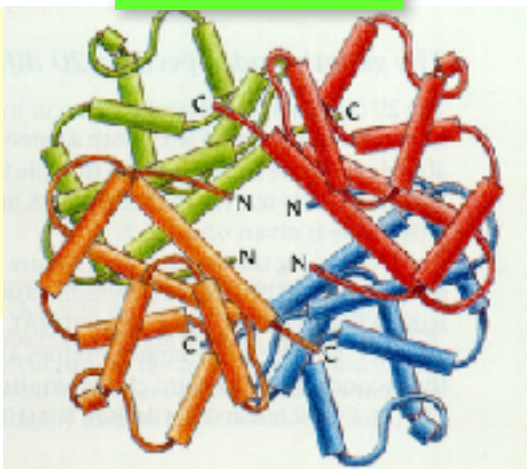


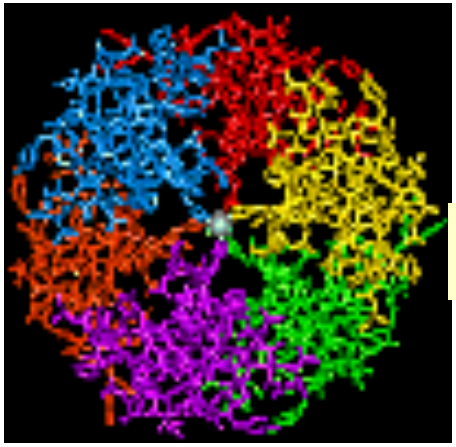
Lambda Cro

Quaternary Structures in Proteins

• The final structure may contain more than one “chain” arranged in a **quaternary structure**.

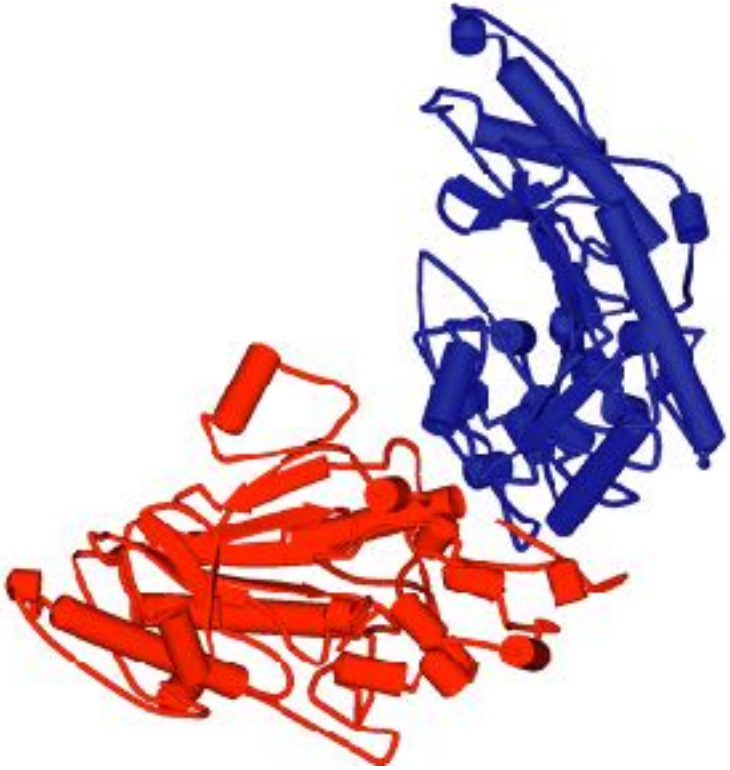
Quaternary





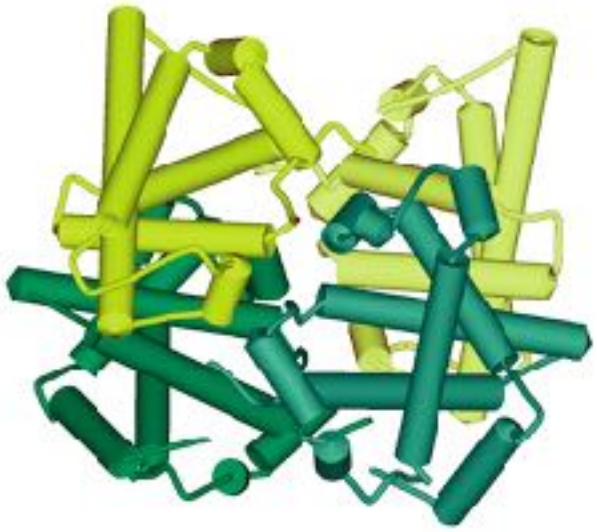
Insulin Hexamer

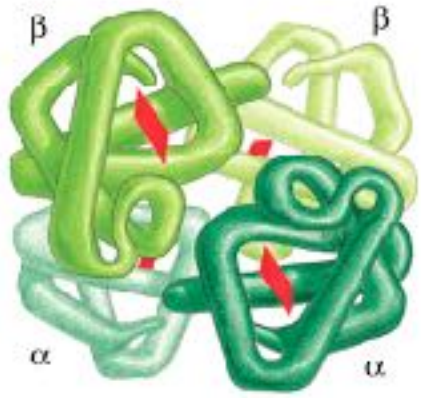
More quaternary structures



Muscle creatine kinase
(Homodimer)

Bovine deoxyhemoglobin
(Heterotetramer)

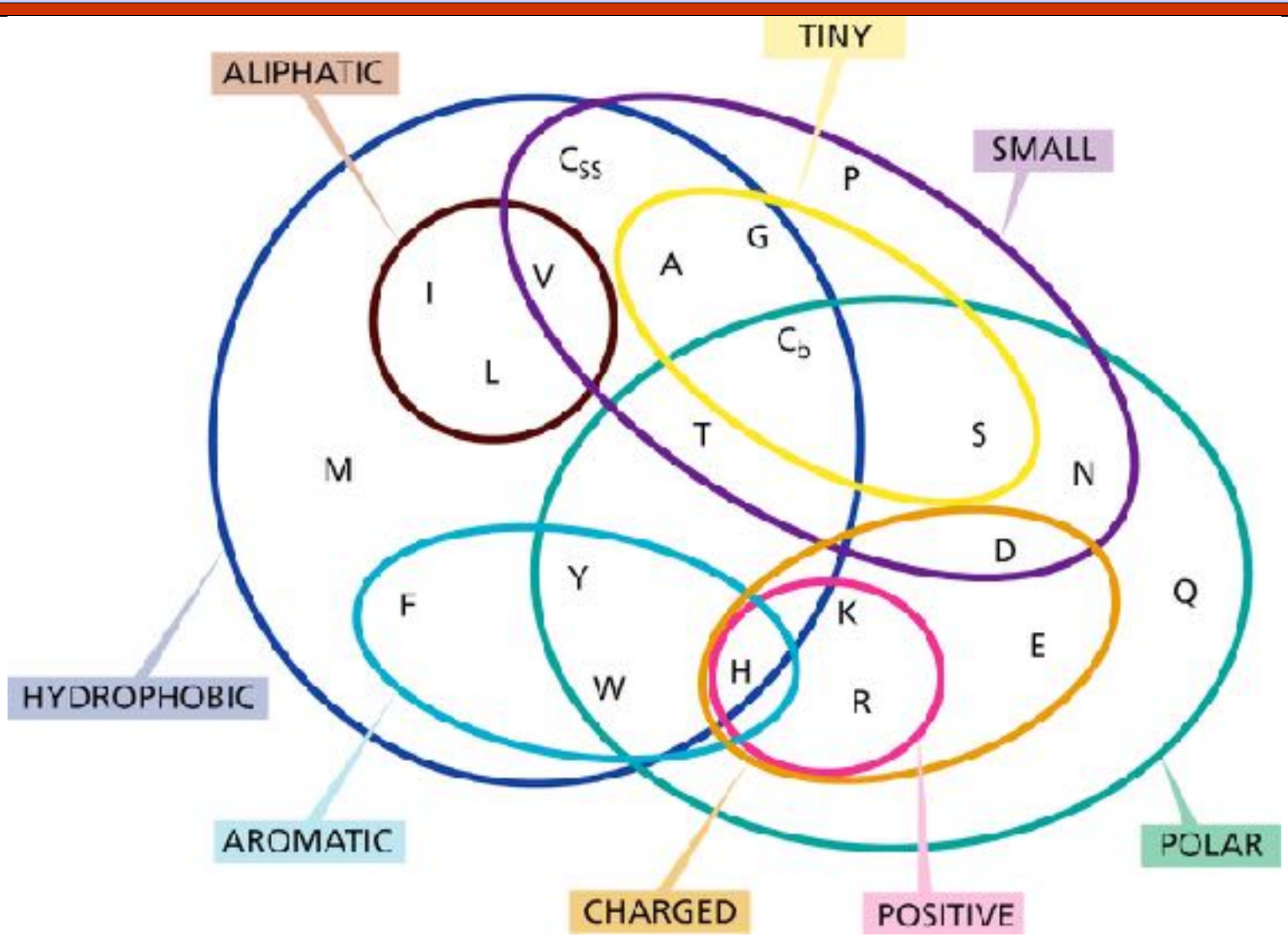




Amino Acid Types

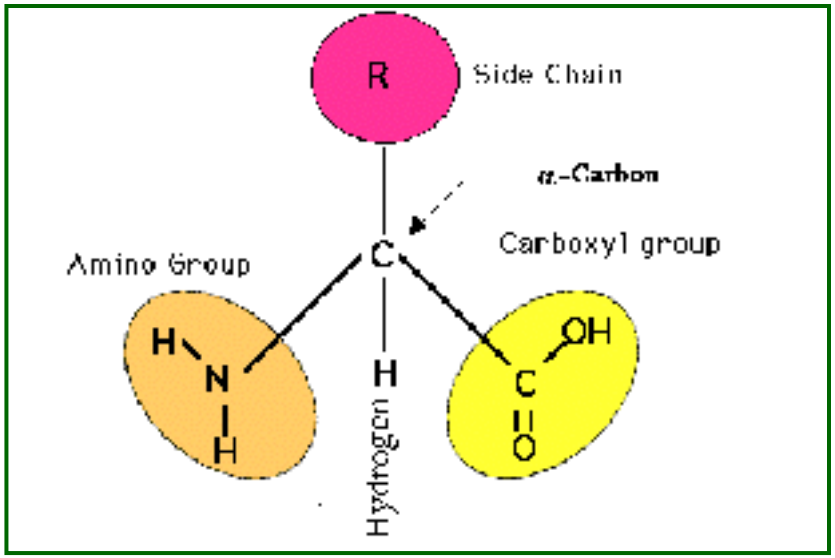
- **Hydrophobic** I,L,M,V,A,F,P
- **Charged**
  - Basic K,H,R
  - Acidic E,D
- **Polar** S,T,Y,H,C,N,Q,W
- **Small** A,S,T
- **Very Small** A,G
- **Aromatic** F,Y,W

Amino Acid Types



Structure of a single amino acid

All 3 figures are cartoons of an amino acid residue.



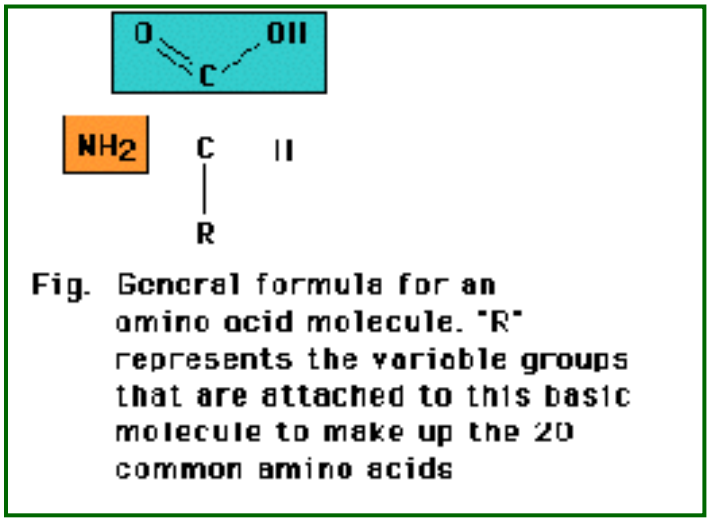
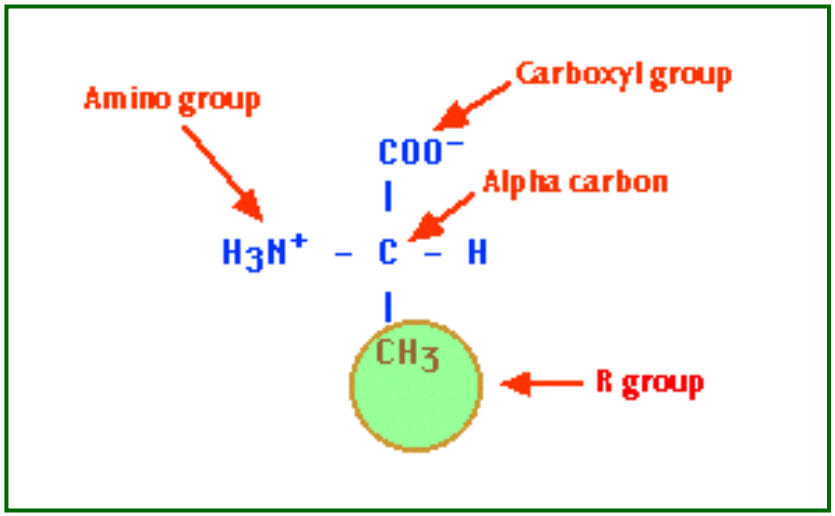
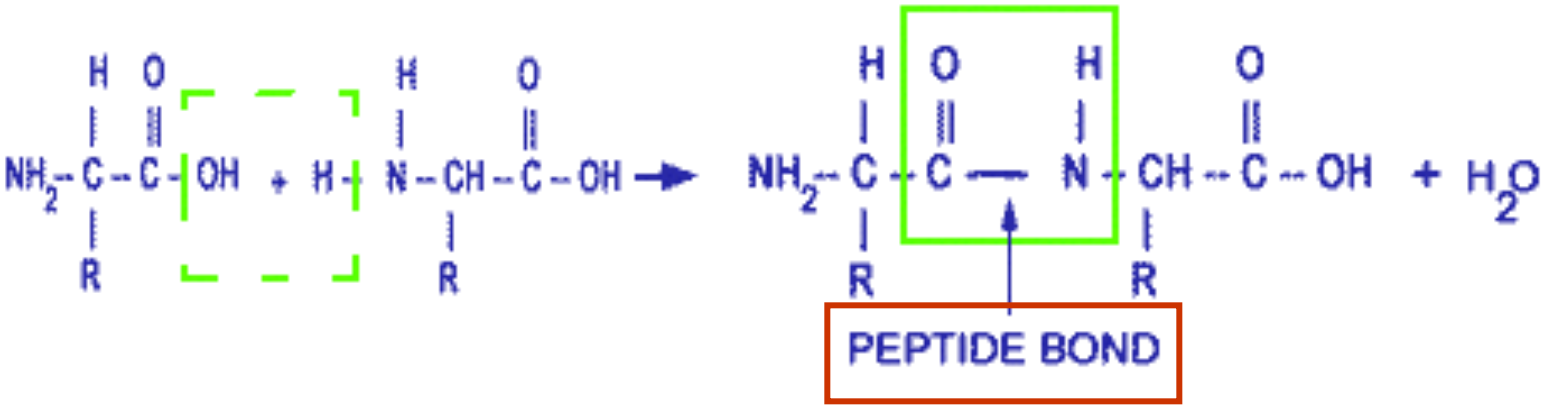


Fig. General formula for an amino acid molecule. "R" represents the variable groups that are attached to this basic molecule to make up the 20 common amino acids



Chains of amino acids



Amino acids vs Amino acid residues

Angles ϕ and ψ in the polypeptide chain

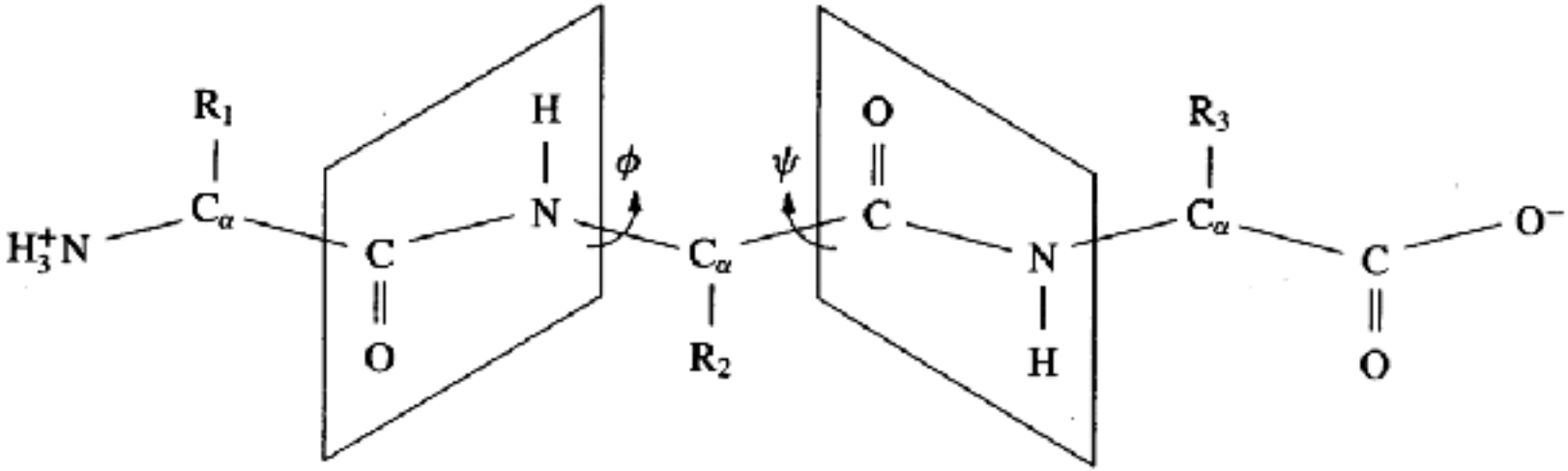
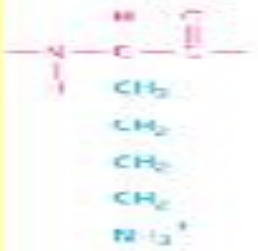


FIGURE 1.2

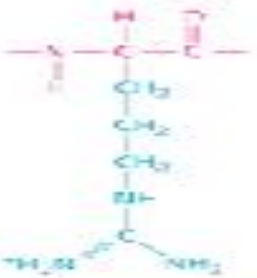
A polypeptide chain. The R_i side chains identify the component amino acids. Atoms inside each quadrilateral are on the same plane, which can rotate according to angles ϕ and ψ.

BASIC SIDE CHAINS

lysine
(Lys, or K)



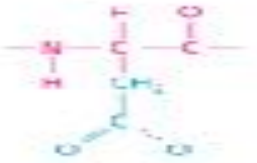
arginine
(Arg, or R)



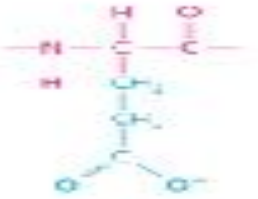
histidine
(His, or H)

ACIDIC SIDE CHAINS

aspartic acid
(Asp, or D)

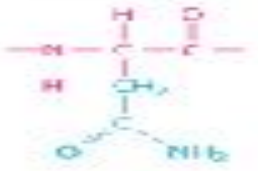


glutamic acid
(Glu, or E)

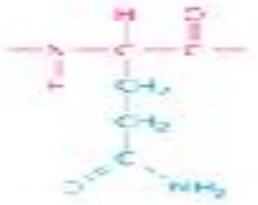


UNCHARGED POLAR SIDE CHAINS

asparagine
(Asn, or N)



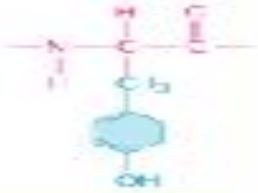
glutamine
(Gln, or Q)



serine
(Ser, or S)

threonine
(Thr, or T)

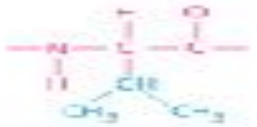
tyrosine
(Tyr, or Y)



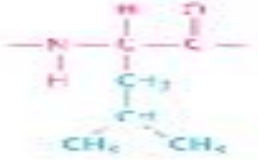
NONPOLAR SIDE CHAINS

alanine
(Ala, or A)

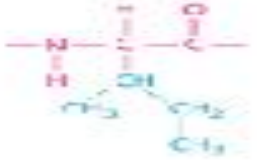
valine
(Val, or V)



leucine
(Leu, or L)



isoleucine
(Ile, or I)

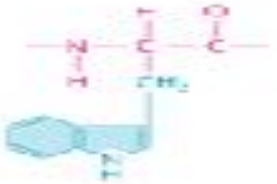


proline
(Pro, or P)

phenylalanine
(Phe, or F)

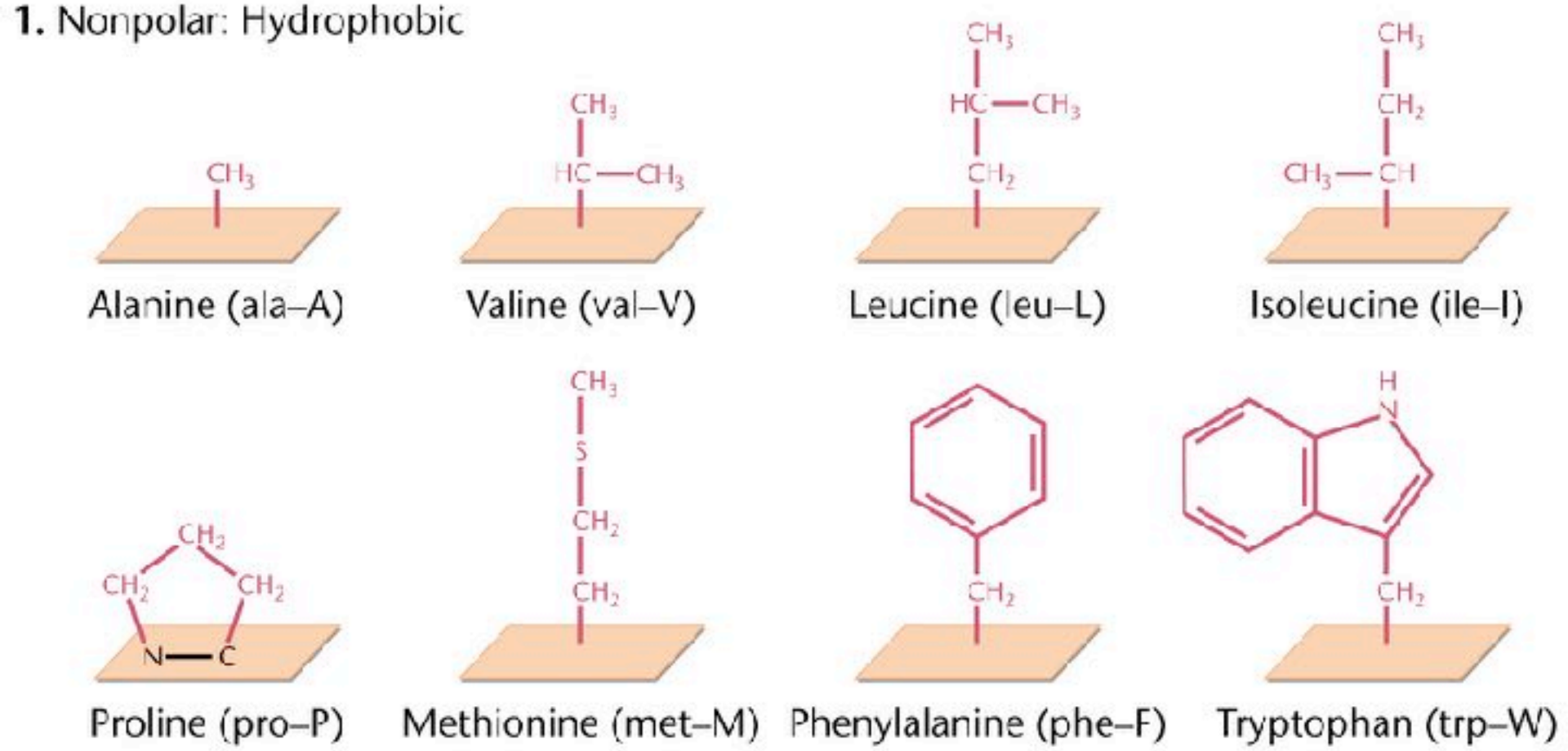
methionine
(Met, or M)

tryptophan
(Trp, or W)



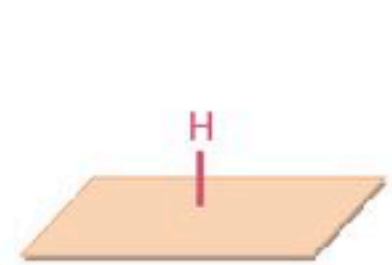
glycine
(Gly, or G)

cysteine
(Cys, or C)

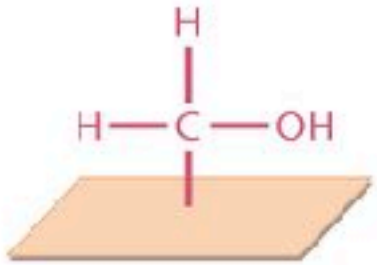


Amino Acid Structures from Klug & Cummings

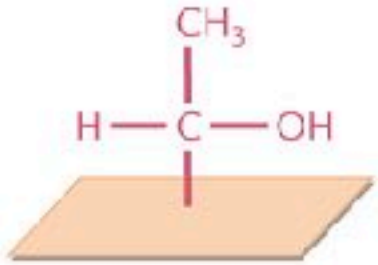
2. Polar: Hydrophilic



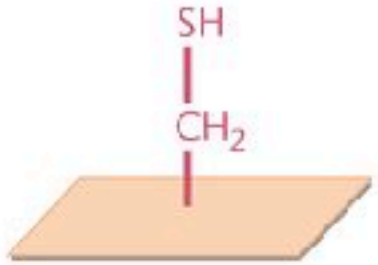
Glycine (gly–G)



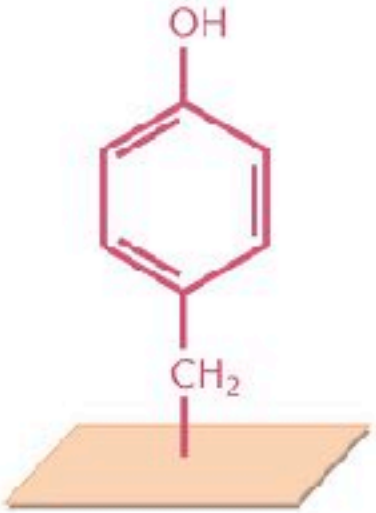
Serine (ser–S)



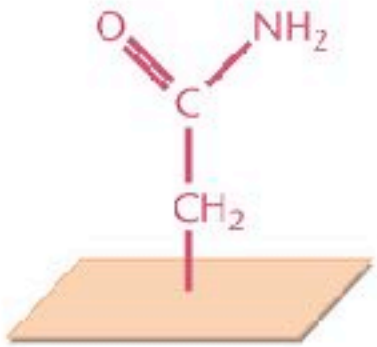
Threonine (thr–T)



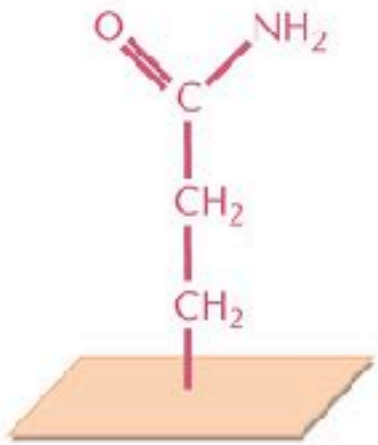
Cysteine (cys–C)



Tyrosine (tyr–Y)



Asparagine (asn–N)

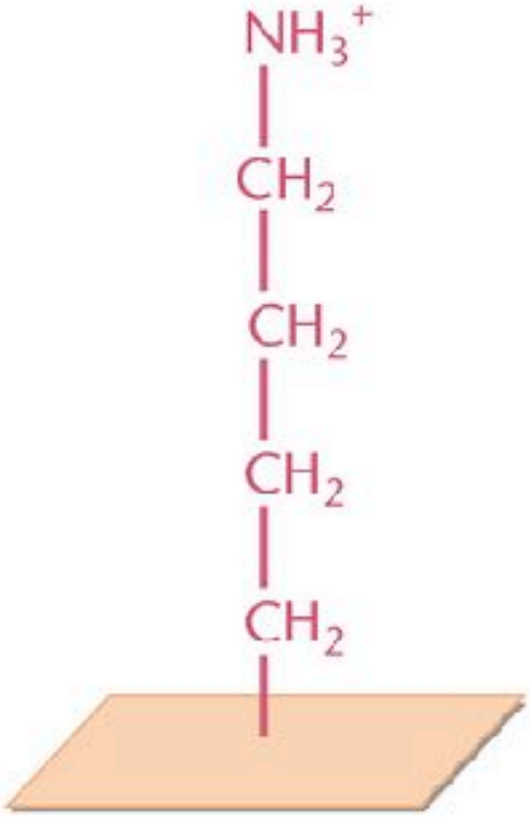


Glutamine (gln–Q)

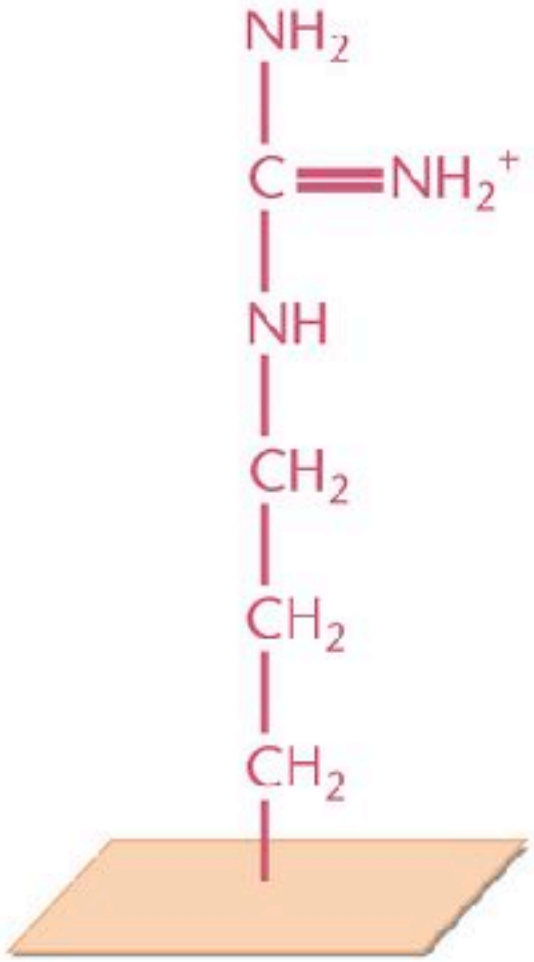
Amino Acid Structures from Klug & Cummings

3. Polar: positively charged (basic)

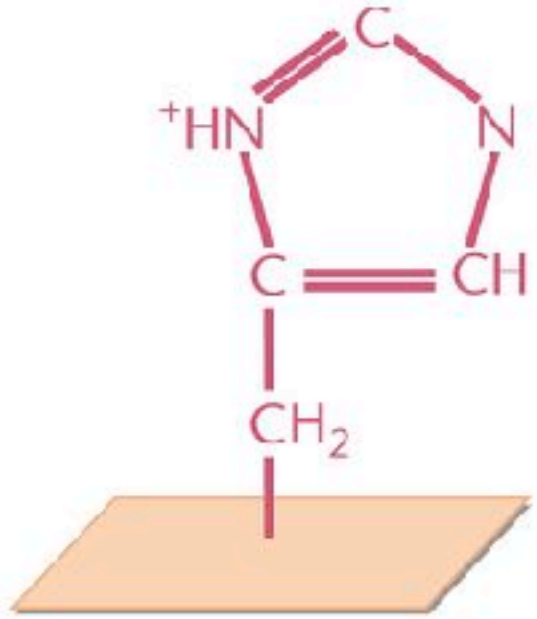
Amino Acid Structures from Klug & Cummings



Lysine (lys–K)

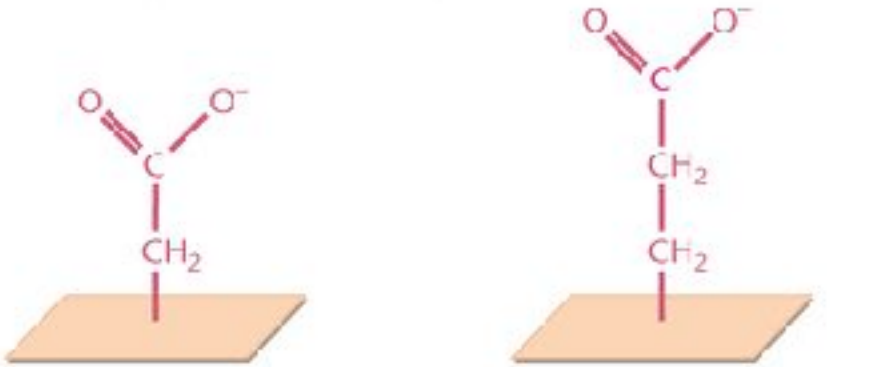


Arginine (arg–R)

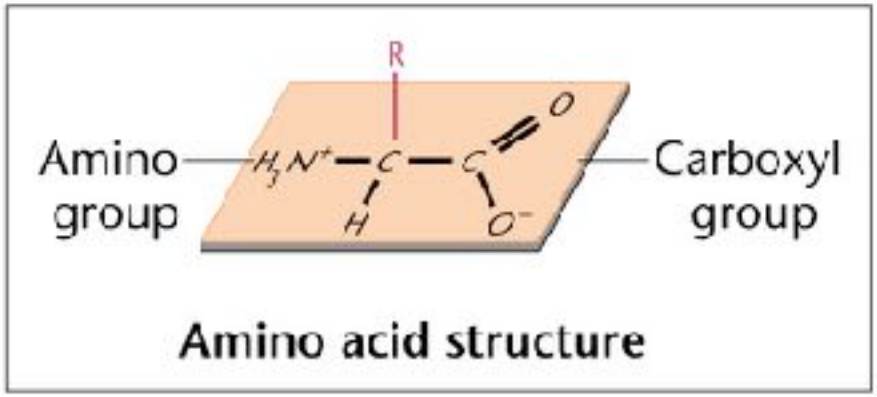


Histidine (his–H)

4. Polar: negatively charged (acidic)



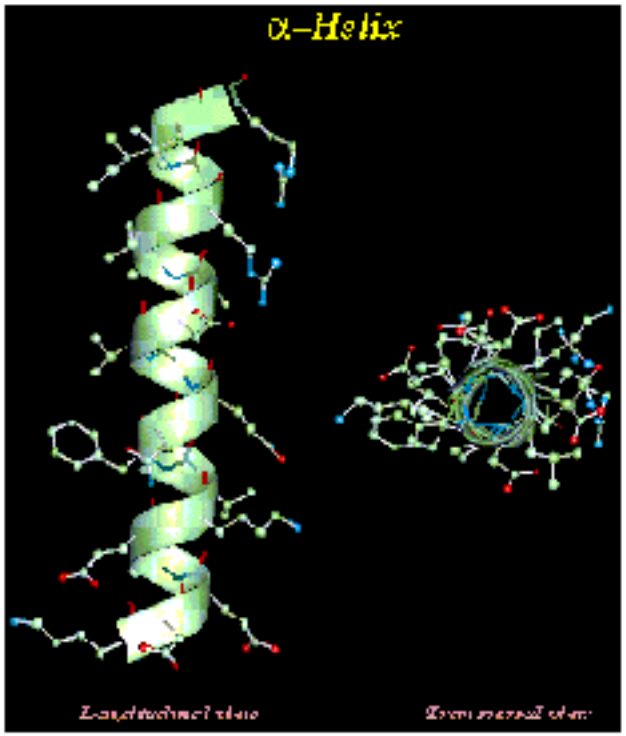
Aspartic acid (asp–D) Glutamic acid (glu–E)

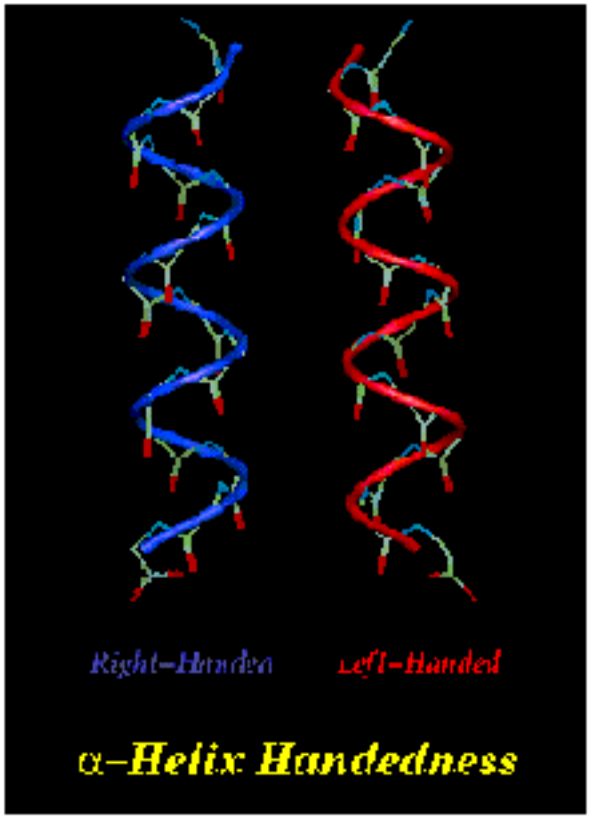


Amino acid structure

Amino Acid Structures from Klug & Cummings

Alpha helices





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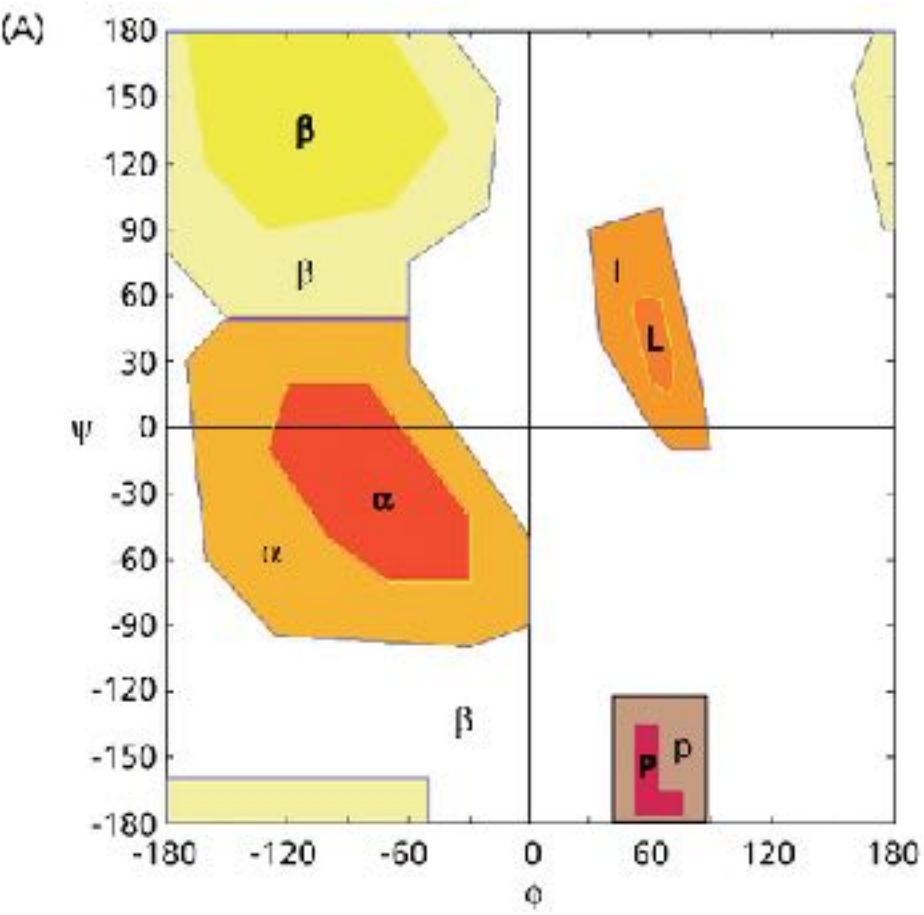
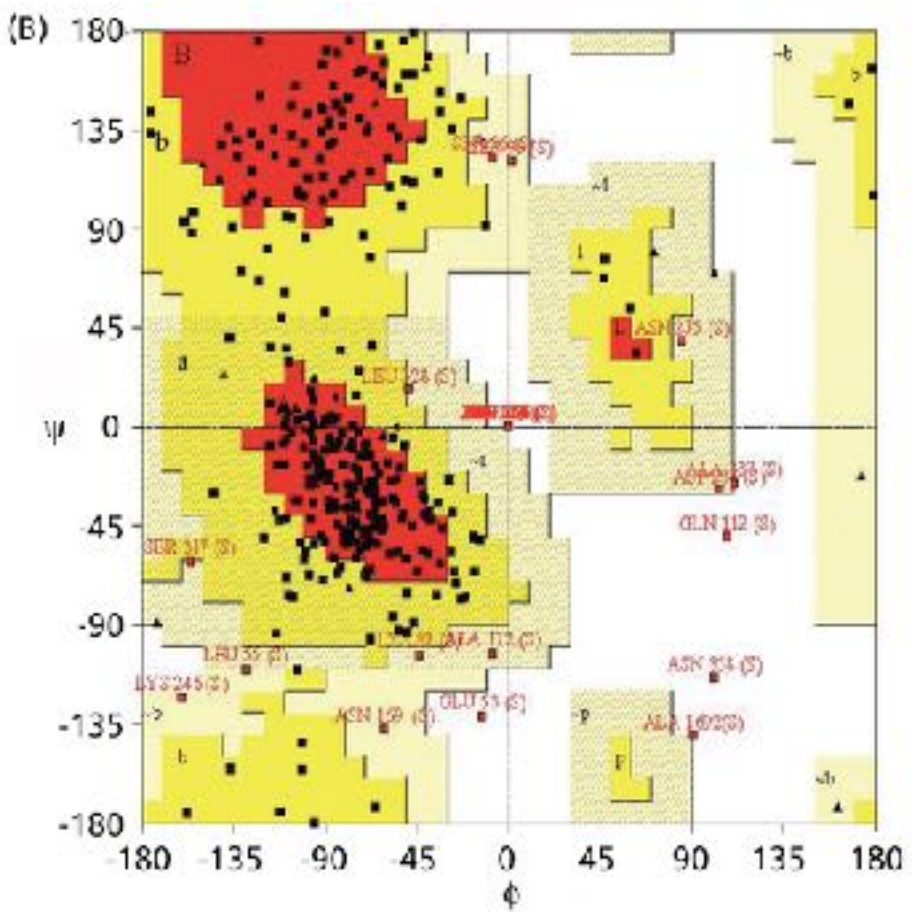
Ramachandran Plot





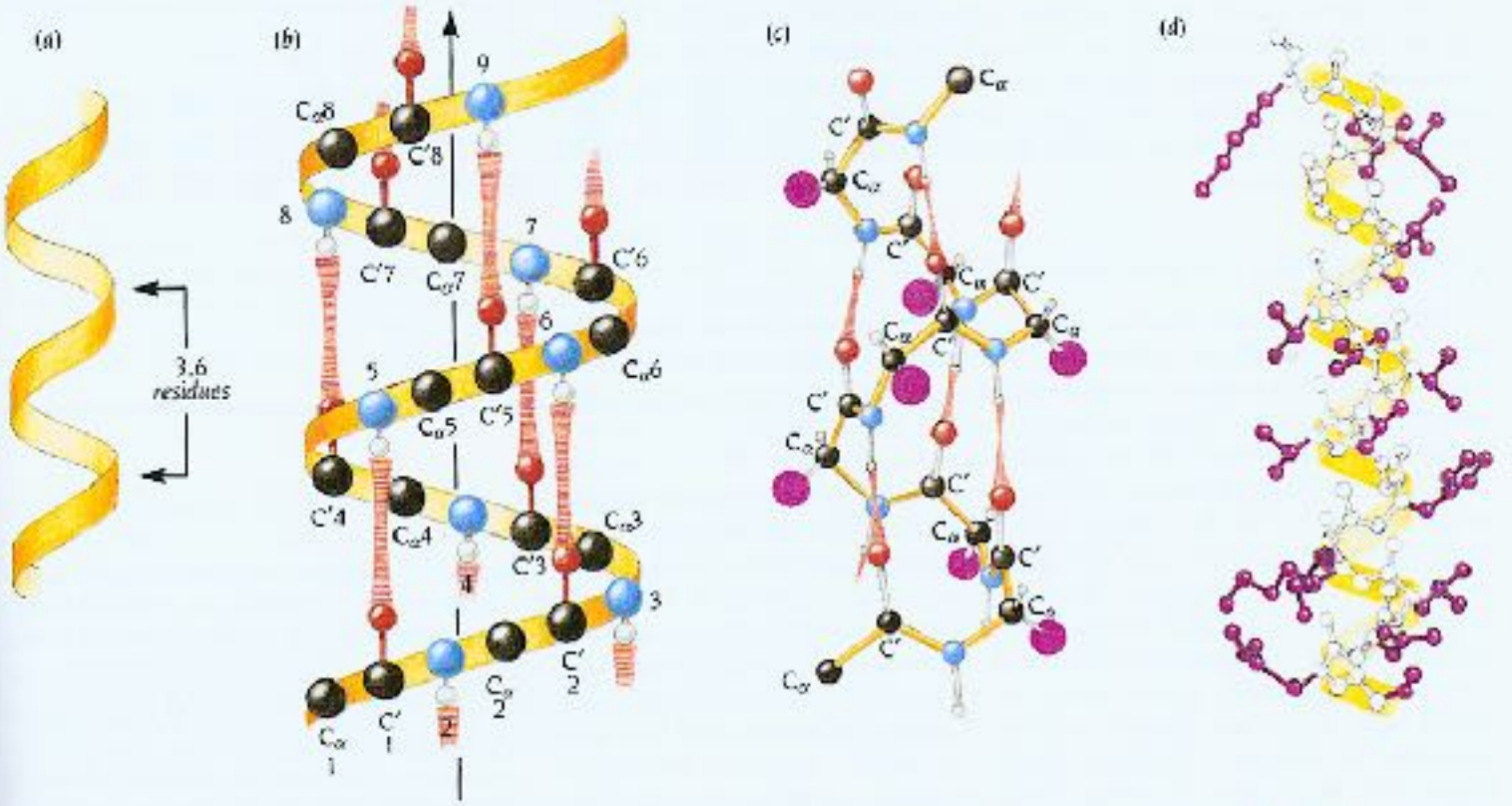
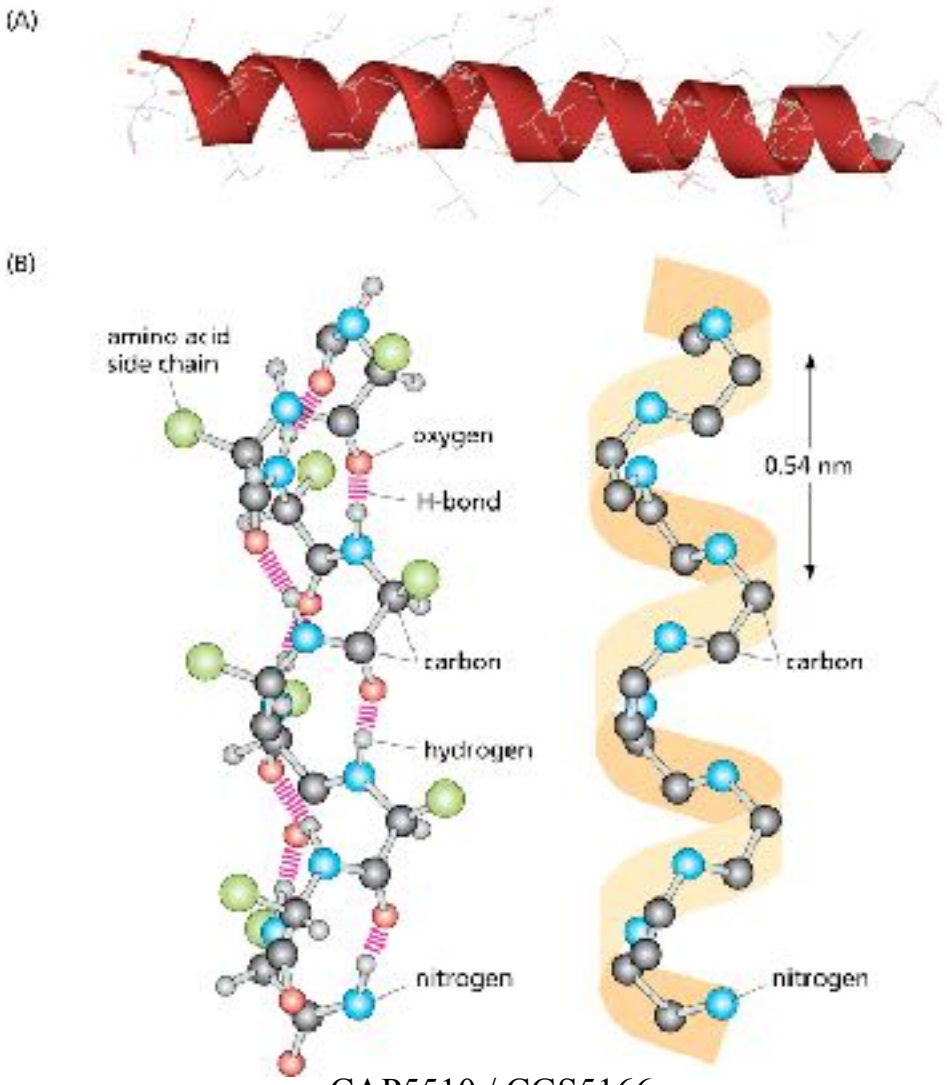
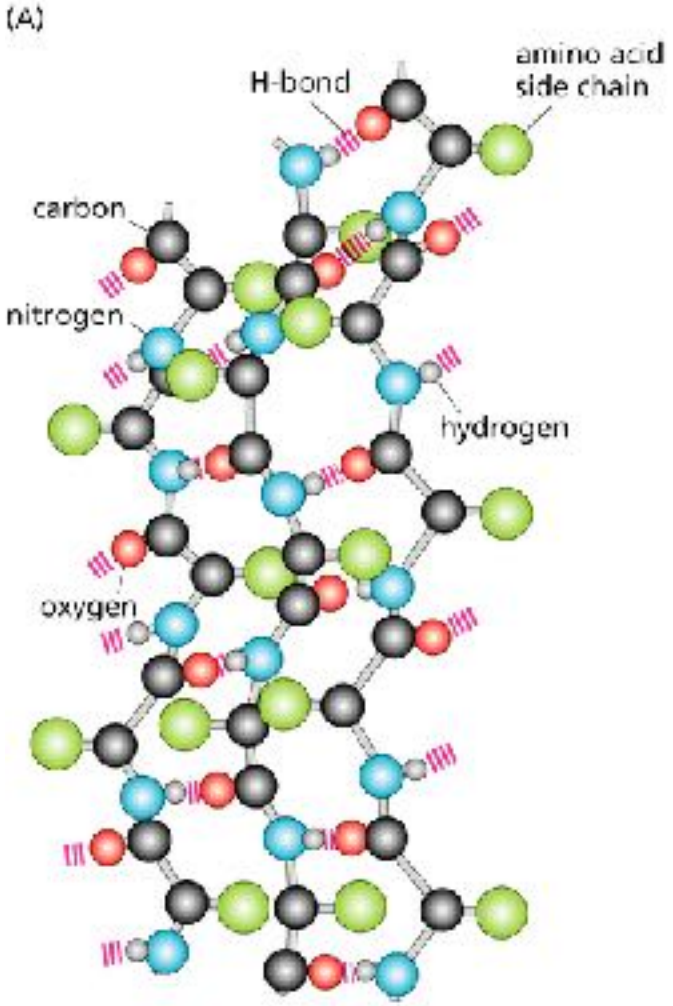


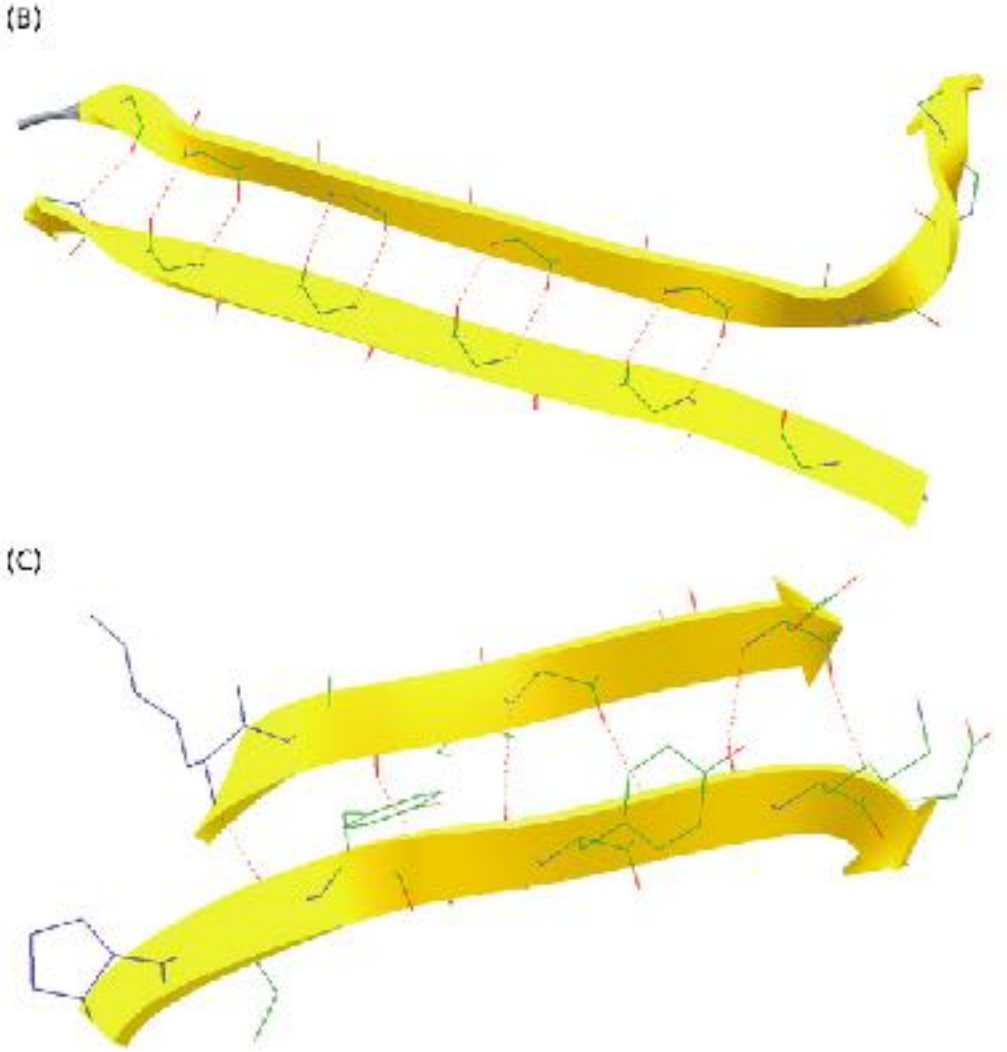
Figure 2.2 The α helix is one of the major elements of secondary structure in proteins. Main-chain N and O atoms are hydrogen-bonded to each other within α helices. (a) Idealized diagram of the path of the main chain in an α helix. Alpha helices are frequently illustrated in this way. There are 3.6 residues per turn in an α helix, which corresponds to 5.4 Å (1.5 Å per residue). (b) The same as (a) but with approximate positions for main-chain atoms and hydrogen bonds included. The arrow denotes the direction from the N-terminus to the C-terminus. (c) Schematic diagram of an α helix. Oxygen atoms are red, and N atoms are blue. Hydrogen bonds between O and N are red and striated. The side chains are represented as purple circles. (d) A ball-and-stick model of one α helix in myoglobin. The path of the main chain is outlined in yellow; side chains are purple. Main-chain atoms are not colored. (e) One turn of an α helix viewed down the helical axis. The purple side chains project out from the α helix.

Alpha Helix

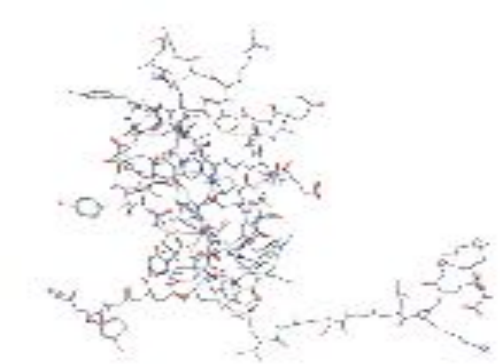

(A)
(B)
amino acid side chain
oxygen
H-bond
carbon
hydrogen
nitrogen
0.54 nm
carbon
nitrogen

Beta Strands and Sheets

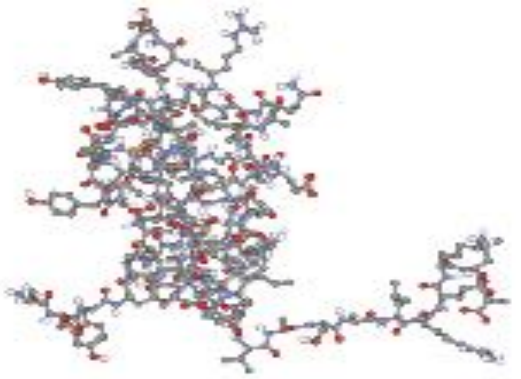




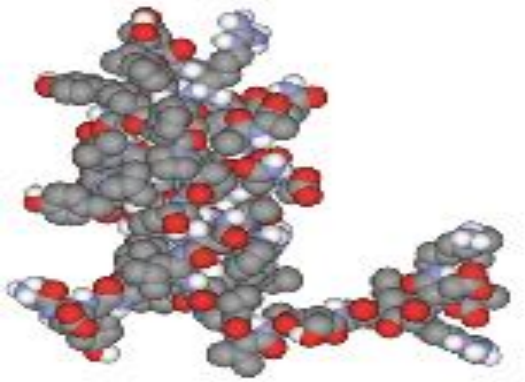
Molecular Representations



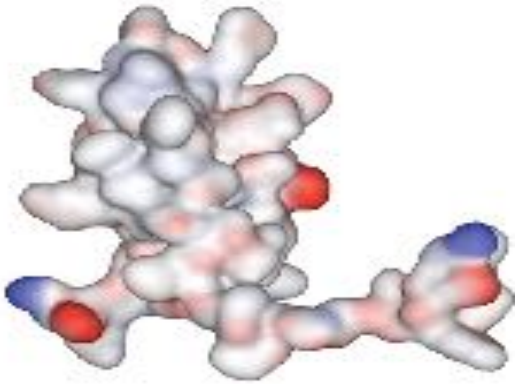
wire-frame



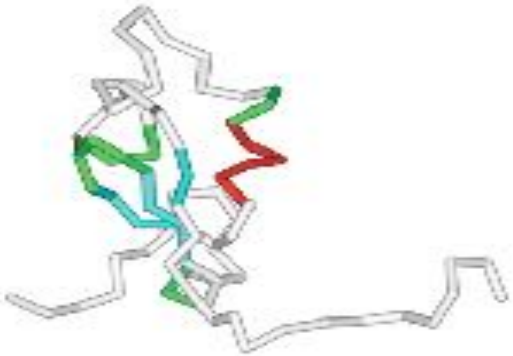
ball and stick



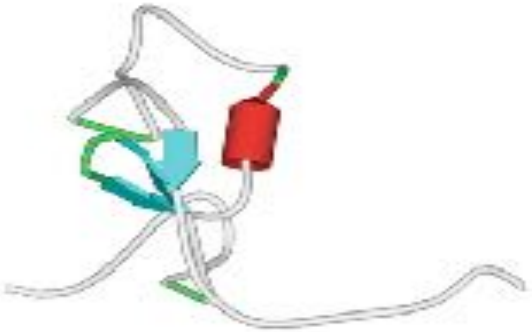
space-filling



surface



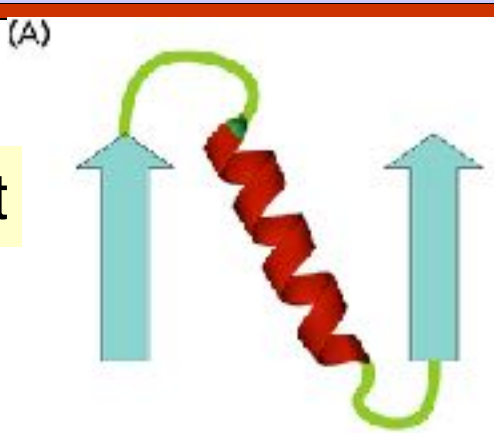
C_β representation

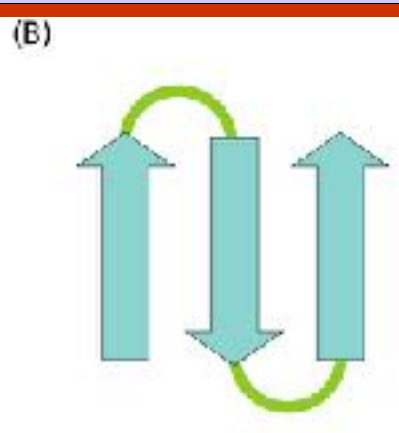


α/β schematic

Supersecondary structures

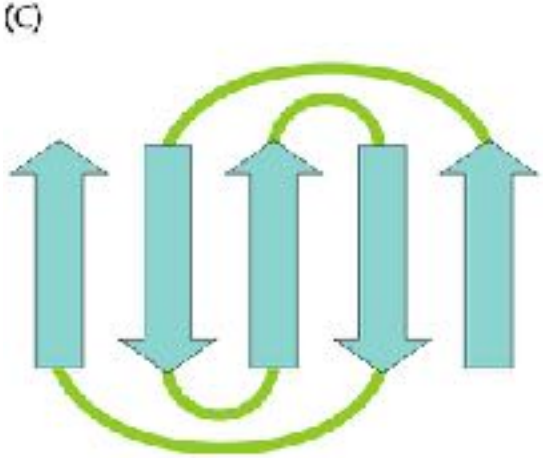
βαβ repeat

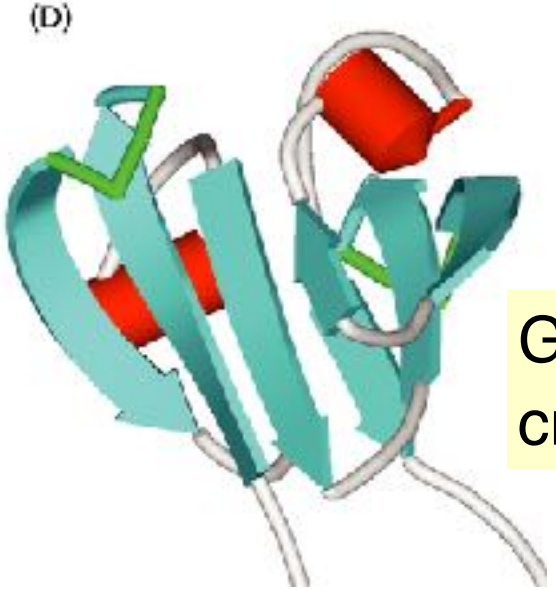




βαβ-meander

Greek Key





Gamma β crystallin

Secondary Structure Prediction Software

Figure 11.3 Comparison of secondary structure predictions by various methods. The sequence of flavodoxin, an α/β protein, was used as the query and is shown on the first line of the alignment. For each prediction, H denotes an α helix, E a β strand, T a β turn; all other positions are assumed to be random coil. Correctly assigned residues are shown in inverse type. The methods used are listed along the left side of the alignment and are described in the text. At the bottom of the figure is the secondary structure assignment given in the PDB file for flavodoxin (1DFV, Smith et al., 1983).

Recent Ones:

GOR V

PREDATOR

Zpred

PROF

NNSSP

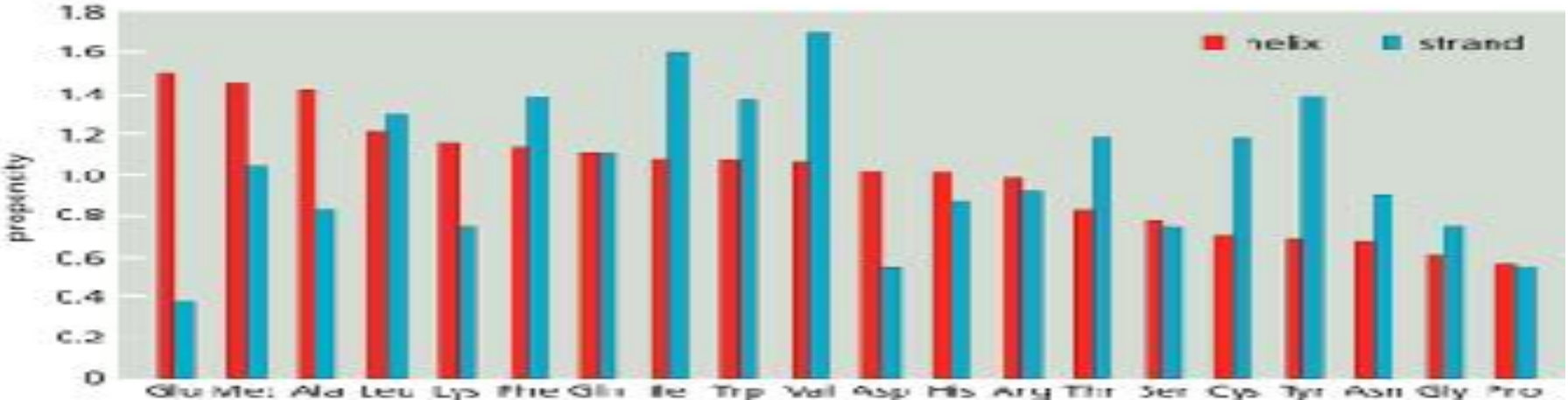
PHD

PSIPRED

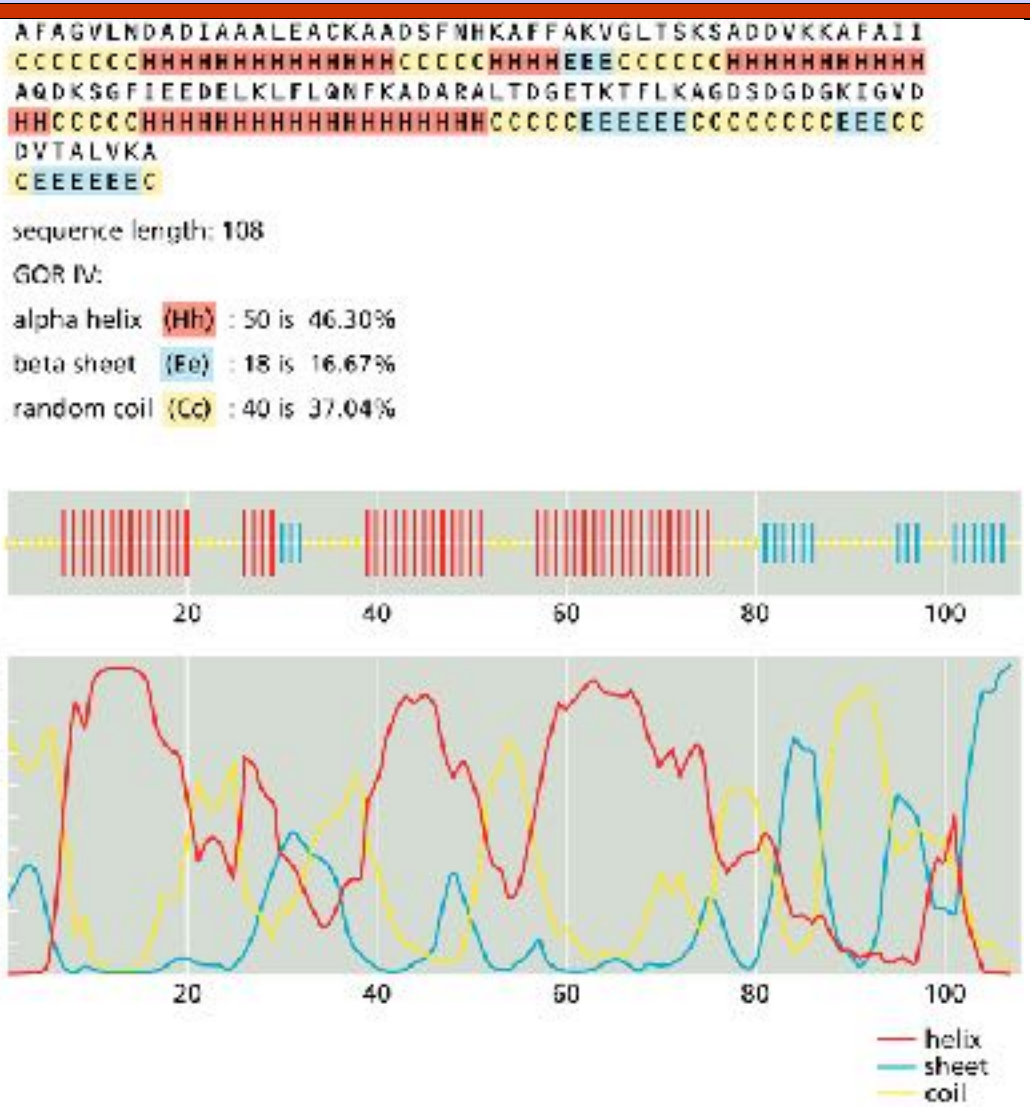
Jnet

Chou & Fasman Propensities

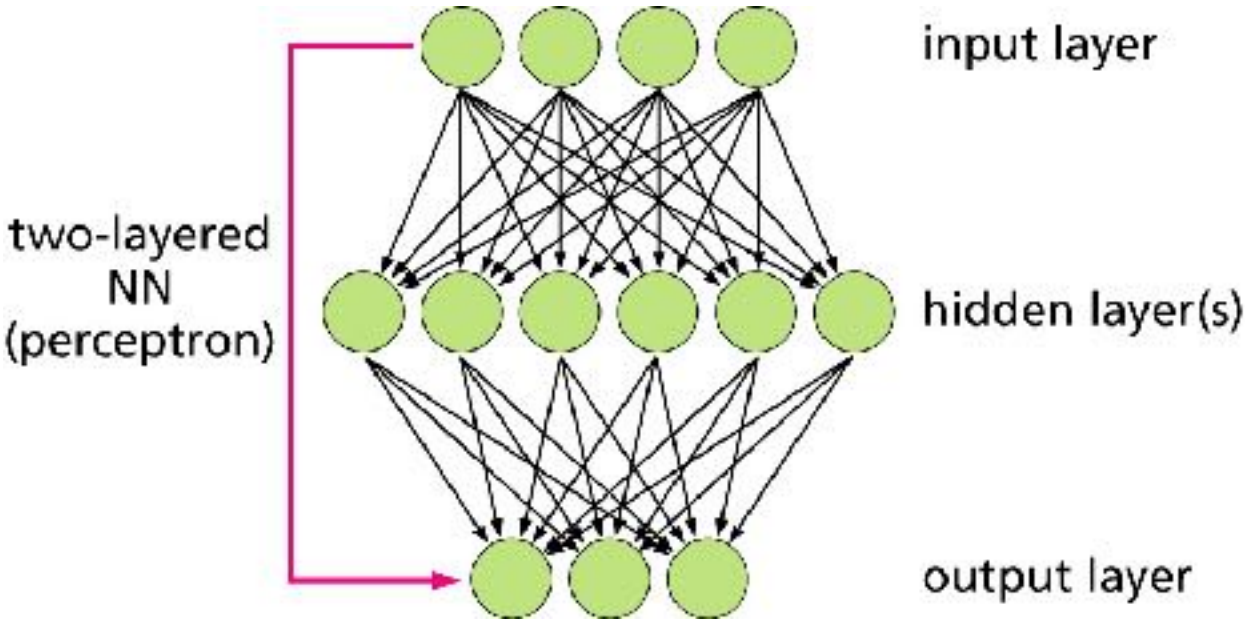
Amino Acid	helix			
	Designation	P	Designation	P
Ala	F	'.42	b	0.83
Cys	I	0.70	f	1.19
Asp	I	'.01	B	0.54
Glu	F	.51	B	0.37
Phe	f	'.13	!	1.33
Gly	B	0.61	b	0.75
His	f	'.00	f	0.87
Ile	f	'.08	F	1.60
Lys	f	'.16	b	0.74
Leu	F	'.21	f	1.30
Met	F	'.45	f	1.05
Asn	b	0.67	b	0.89
Pro	B	0.57	B	0.55
Gln	f	'.11	h	1.10
Arg	I	0.98	I	0.93
Ser	I	0.77	b	0.75
Thr	I	0.83	f	1.19
Val	f	'.06	F	1.70
Trp	f	'.08	f	1.37
Tyr	b	0.69	F	1.47



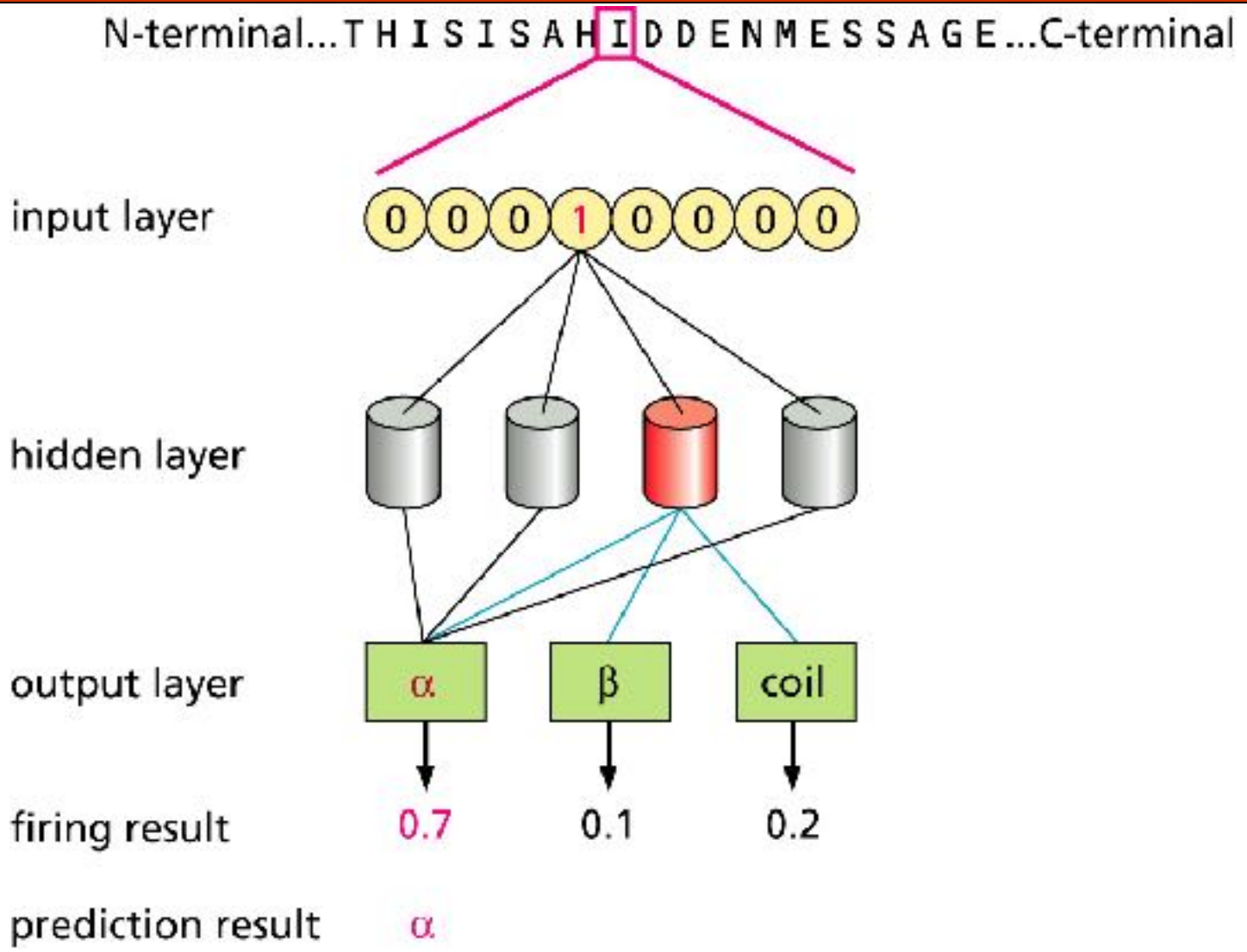
GOR IV prediction for 1bbc



Neural Networks



Neural Network Prediction of SS

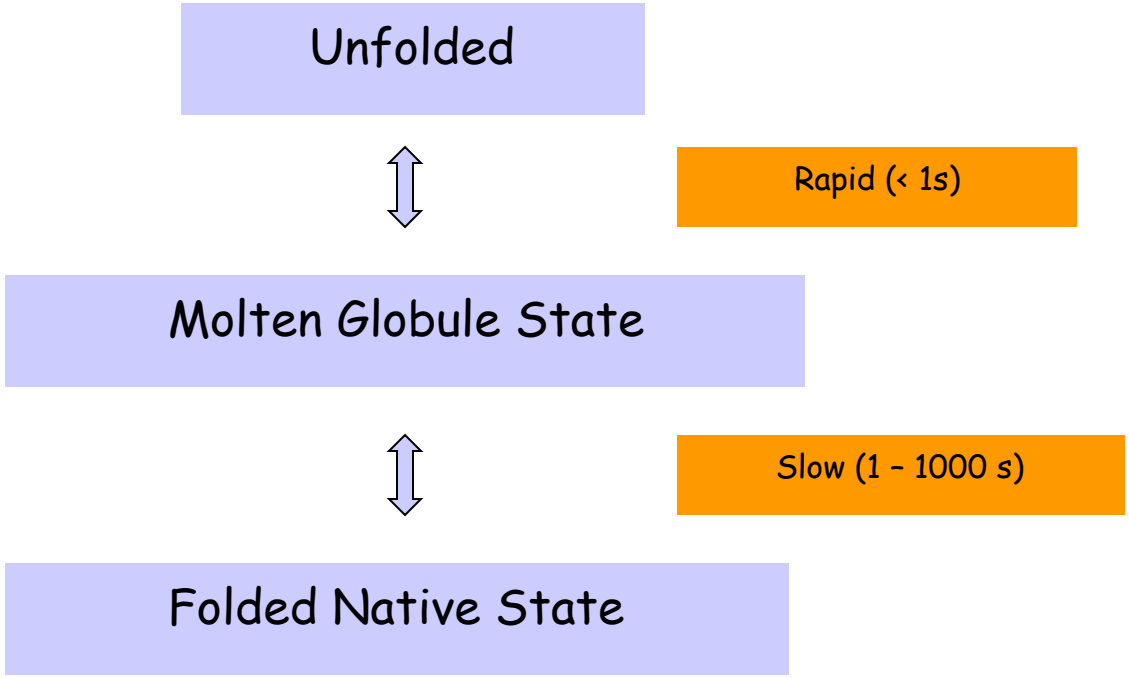


PDB: Protein Data Bank

- Database of protein tertiary and quaternary structures and protein complexes. http://www.rcsb.org/pdb/
- Over 29,000 structures as of Feb 1, 2005.
- Structures determined by
  - NMR Spectroscopy
  - X-ray crystallography
  - Computational prediction methods
- Sample PDB file: Click here [ ]

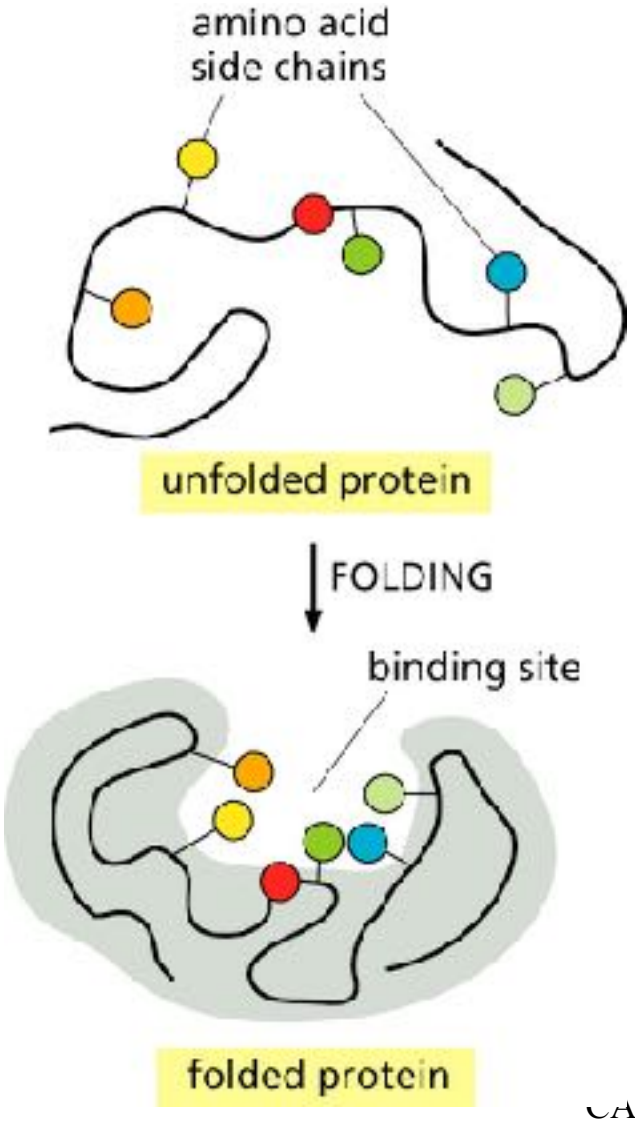
PDB Search Results

Protein Folding

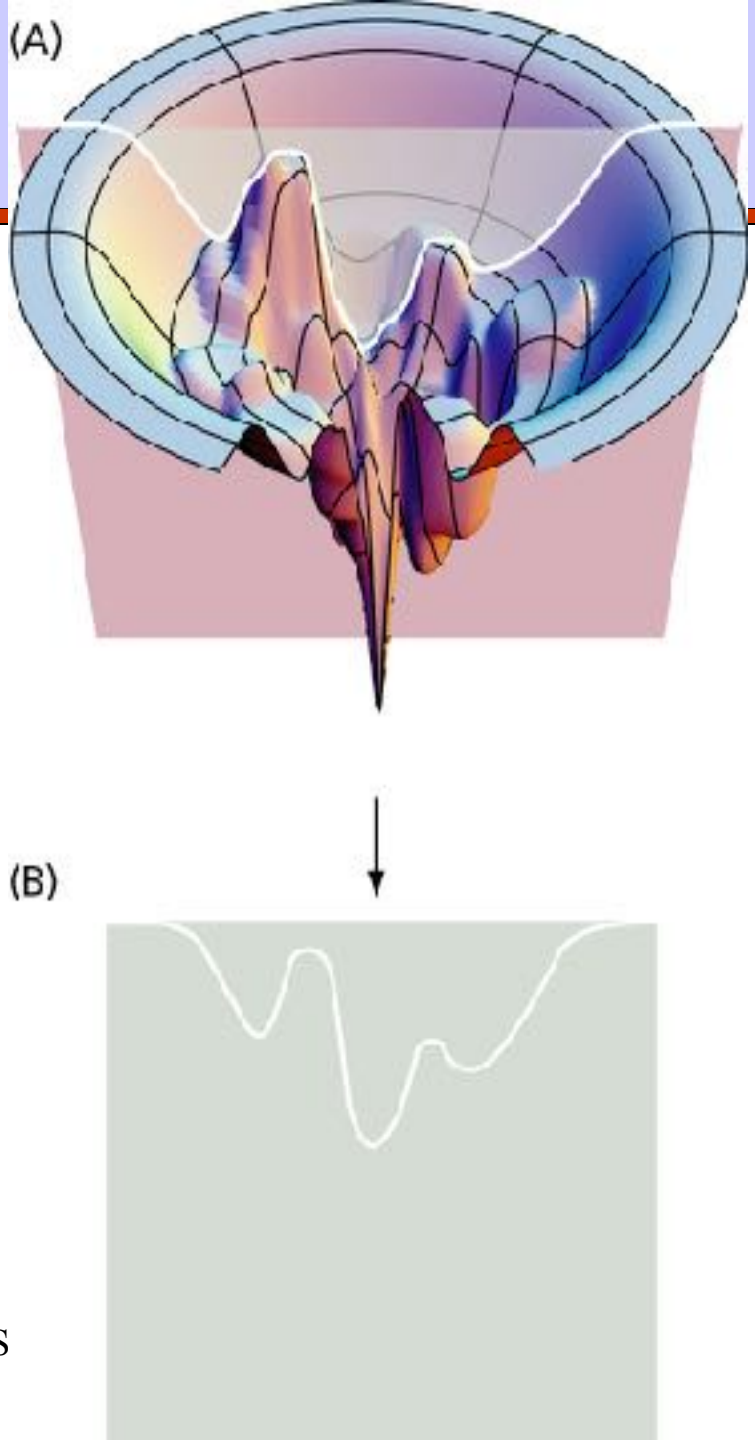


- How to find minimum energy configuration?

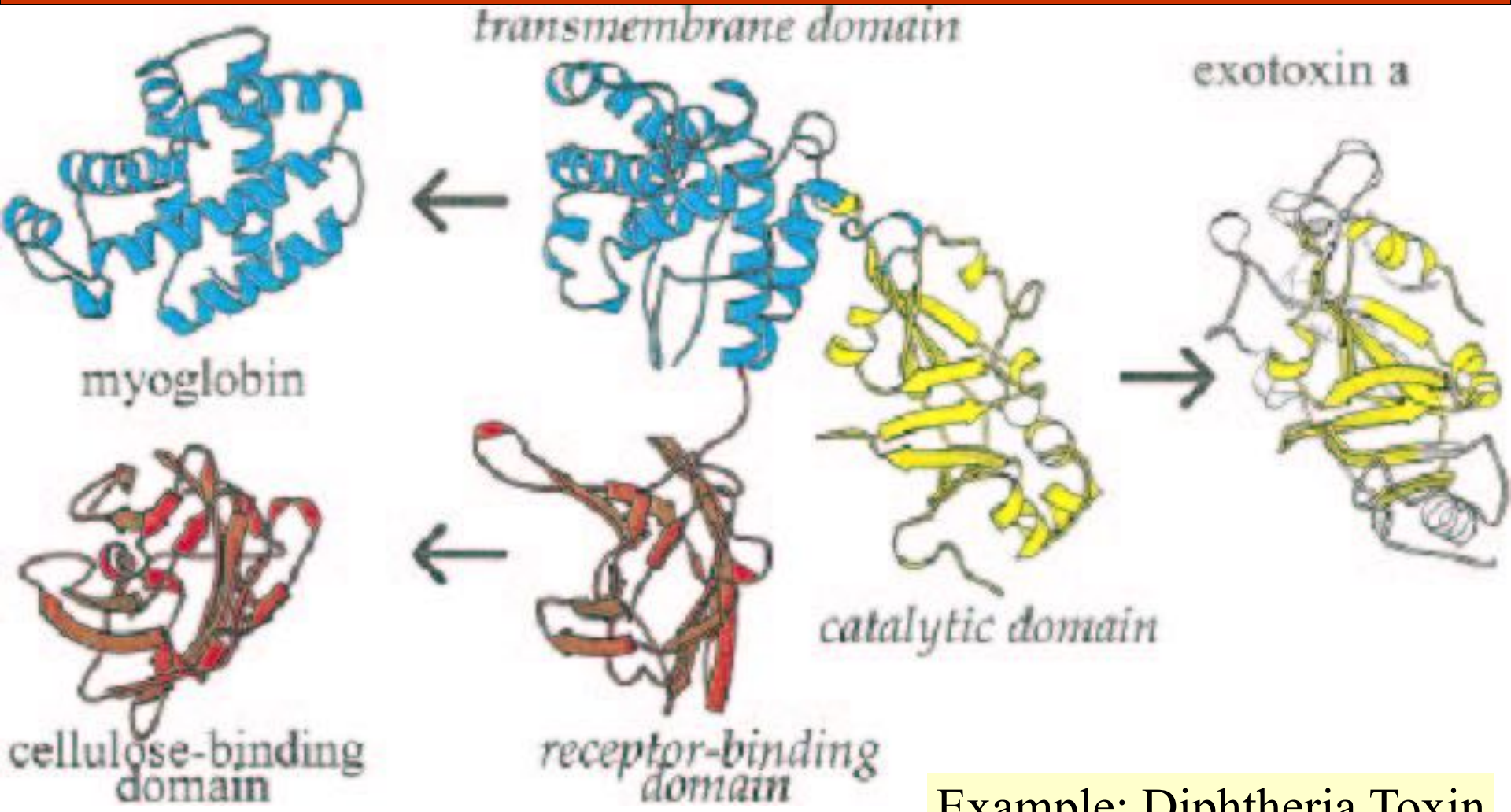
Protein Folding



Energy Landscape



Modular Nature of Protein Structures



Example: Diphtheria Toxin

Protein Structures

- Most proteins have a hydrophobic core.
- Within the core, specific interactions take place between amino acid side chains.
- Can an amino acid be replaced by some other amino acid?
  - Limited by space and available contacts with nearby amino acids
- Outside the core, proteins are composed of loops and structural elements in contact with water, solvent, other proteins and other structures.

Active Sites

Active sites in proteins are usually hydrophobic pockets/ crevices/troughs that involve sidechain atoms.

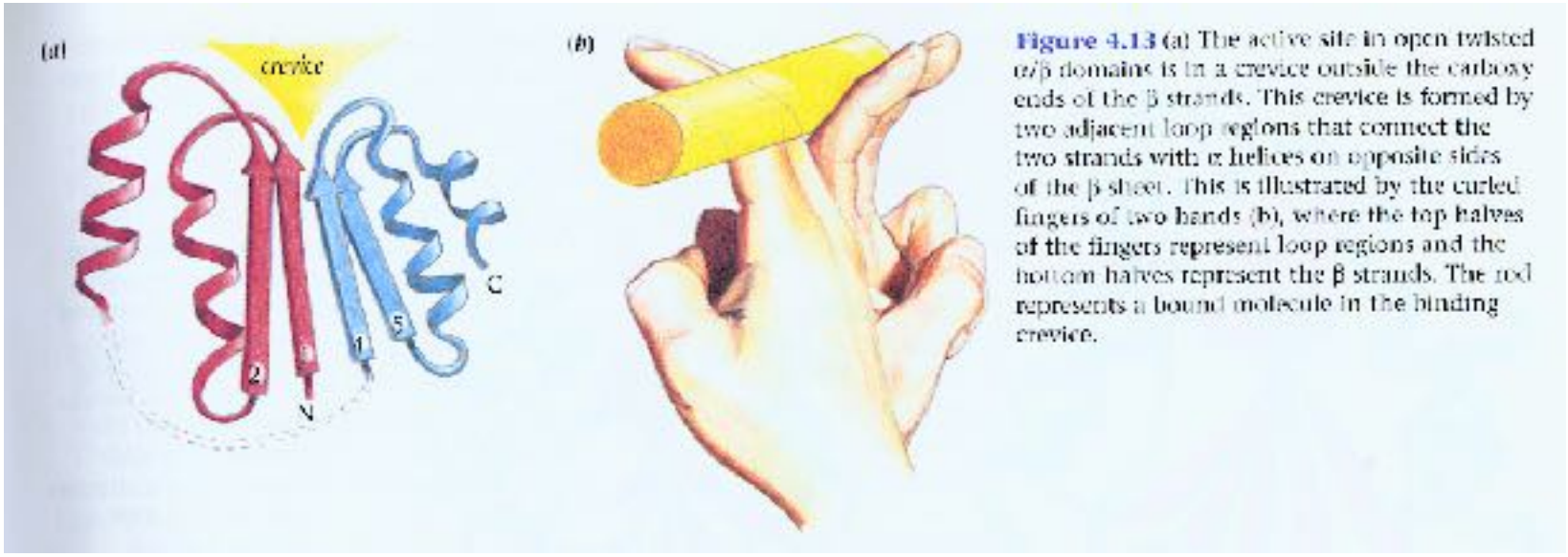
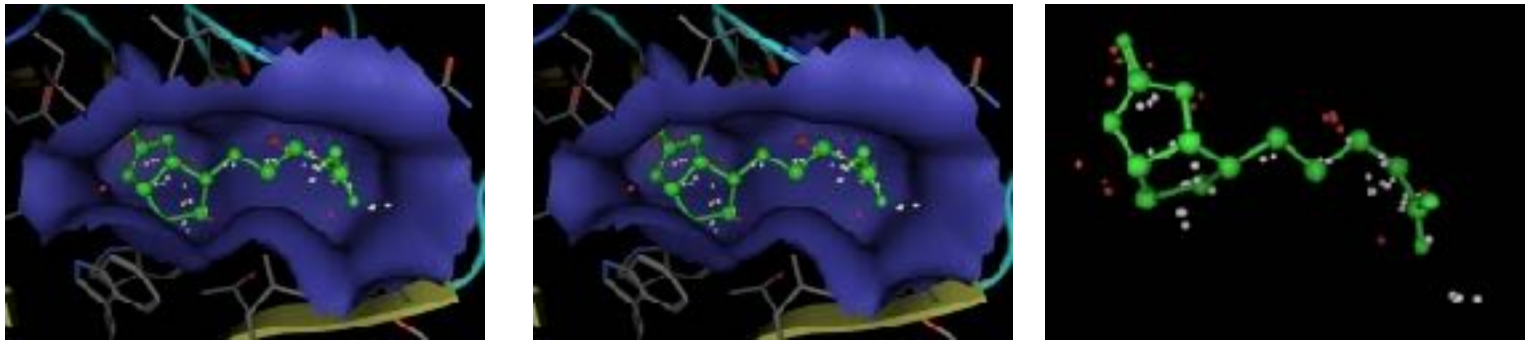


Figure 4.13 (a) The active site in open twisted α/β domains is in a crevice outside the carboxy ends of the β strands. This crevice is formed by two adjacent loop regions that connect the two strands with α helices on opposite sides of the β sheet. This is illustrated by the curled fingers of two hands (b), where the top halves of the fingers represent loop regions and the bottom halves represent the β strands. The rod represents a bound molecule in the binding crevice.

Active Sites



Left PDB 3RTD (streptavidin) and the first site located by the MOE Site Finder. **Middle** 3RTD with complexed ligand (biotin). **Right** Biotin ligand overlaid with calculated alpha spheres of the first site.

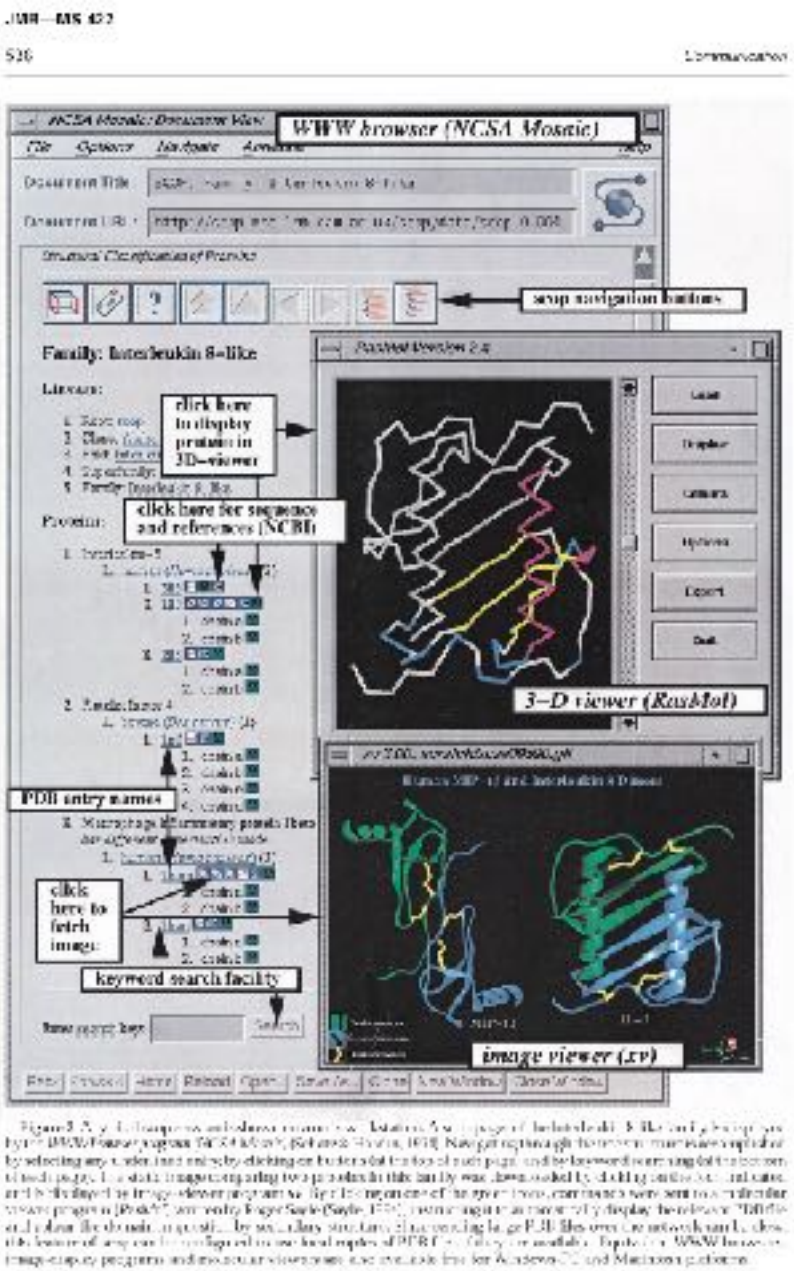
Viewing Protein Structures

- SPDBV
- RASMOL
- CHIME

Structural Classification of Proteins

- Over 1000 protein families known
  - Sequence alignment, motif finding, block finding, similarity search
- SCOP (Structural Classification of Proteins)
  - Based on structural & evolutionary relationships.
  - Contains ~ 40,000 domains
  - Classes (groups of folds), Folds (proteins sharing folds), Families (proteins related by function/evolution), Superfamilies (distantly related proteins)

SCOP Family View



CATH: Protein Structure Classification

- Semi-automatic classification; ~36K domains
- 4 levels of classification:
  - Class (C), depends on sec. Str. Content
    - α class, β class, α/β class, $\alpha+\beta$ class
  - Architecture (A), orientation of sec. Str.
  - Topolgy (T), topological connections &
  - Homologous Superfamily (H), similar str and functions.

DALI/FSSP Database

- Completely automated; 3724 domains
- Criteria of compactness & recurrence
- Each domain is assigned a Domain Classification number DC_l_m_n_p representing fold space attractor region (l), globular folding topology (m), functional family (n) and sequence family (p).

Structural Alignment

- What is structural alignment of proteins?
  - 3-d superimposition of the atoms as "best as possible", i.e., to minimize RMSD (root mean square deviation).
  - Can be done using VAST and SARF
- Structural similarity is common, even among proteins that do not share sequence similarity or evolutionary relationship.

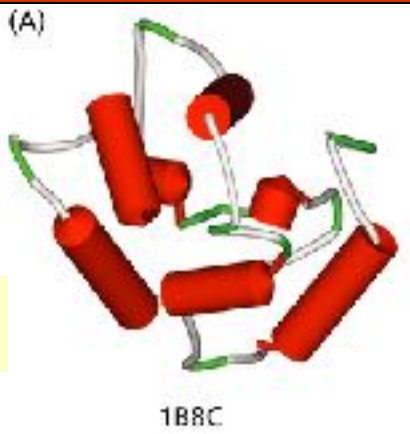
Other databases & tools

- MMDB contains groups of structurally related proteins
- SARF structurally similar proteins using secondary structure elements
- VAST Structure Neighbors
- SSAP uses double dynamic programming to structurally align proteins

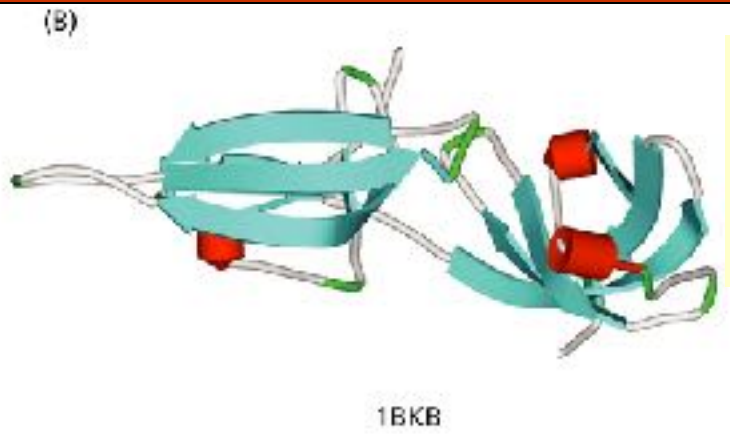
5 Fold Space classes

Attractor 1 can be characterized as alpha/beta,
attractor 2 as all-beta, attractor 3 as all-alpha,
attractor 5 as alpha-beta meander (1mli), and
attractor 4 contains antiparallel beta-barrels e.g. OB-fold (1prtF).

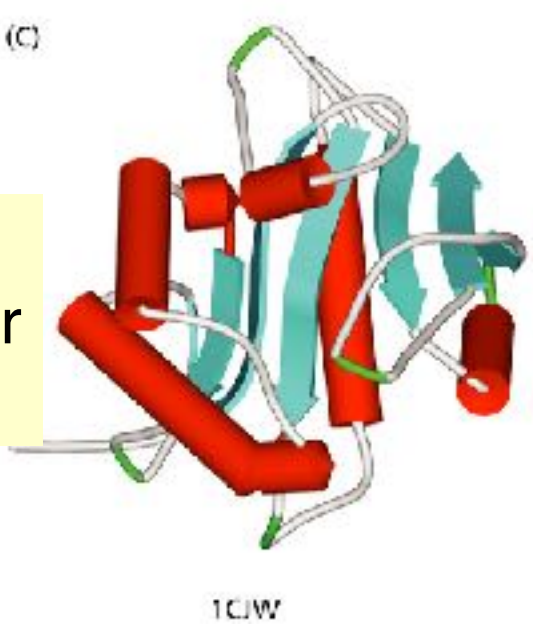
Examples of protein classes



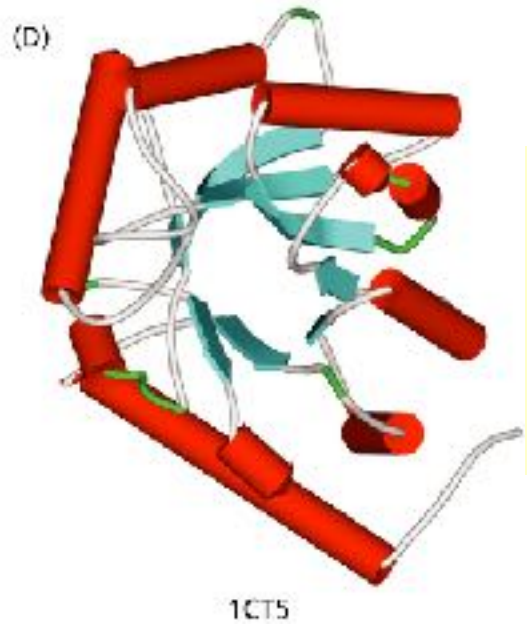
Parvalbumin



Translation Initiation Factor 5A

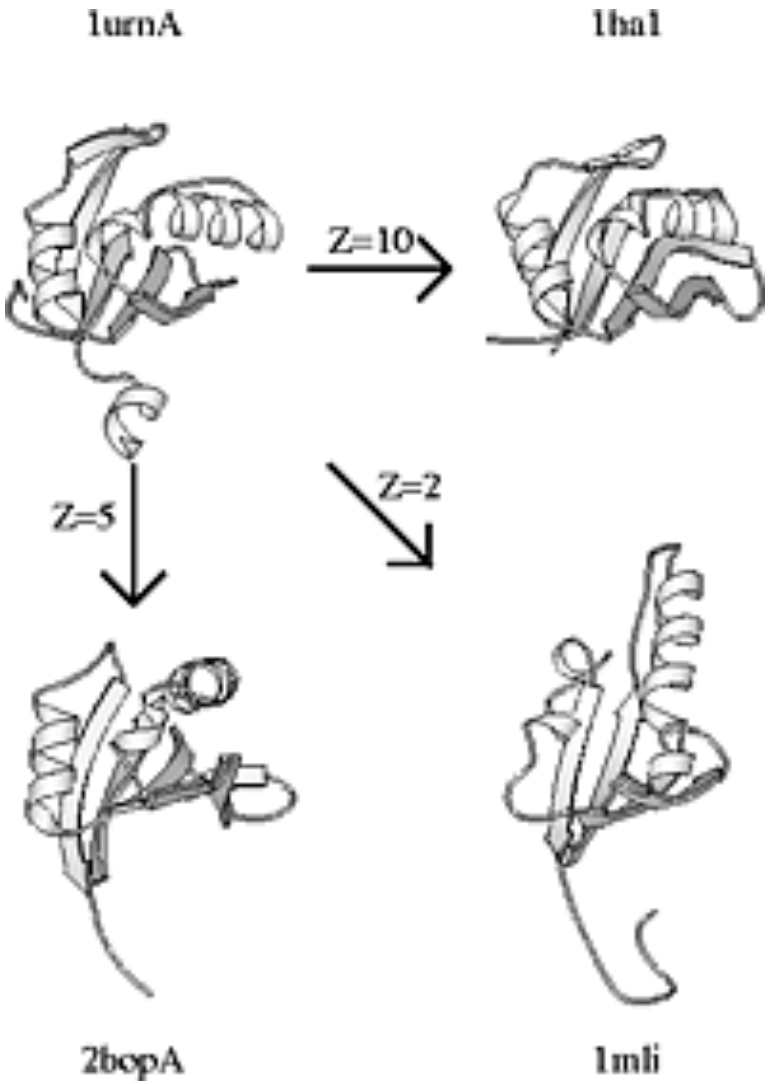


Serotonin N-acetyltransferase



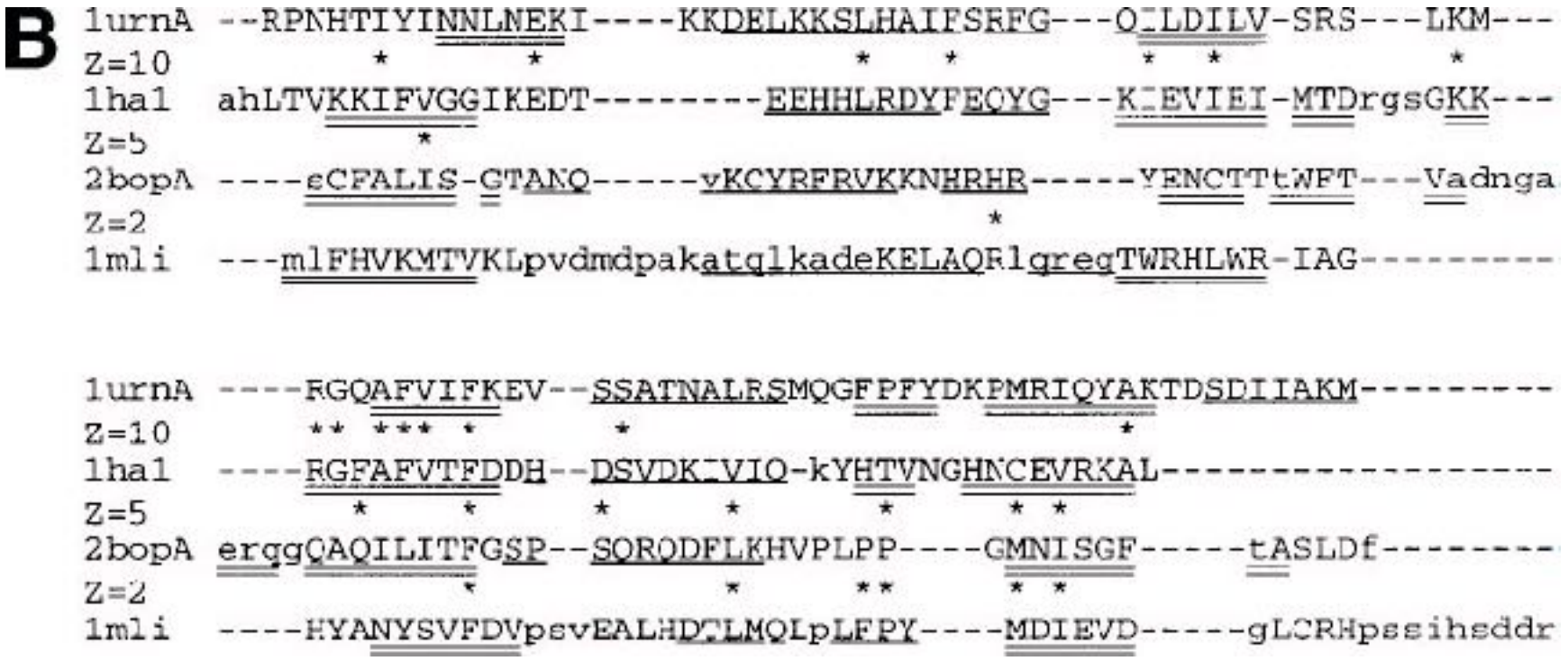
Hypothetical protein from yeast (α/β alternating fold)

Fold Types & Neighbors

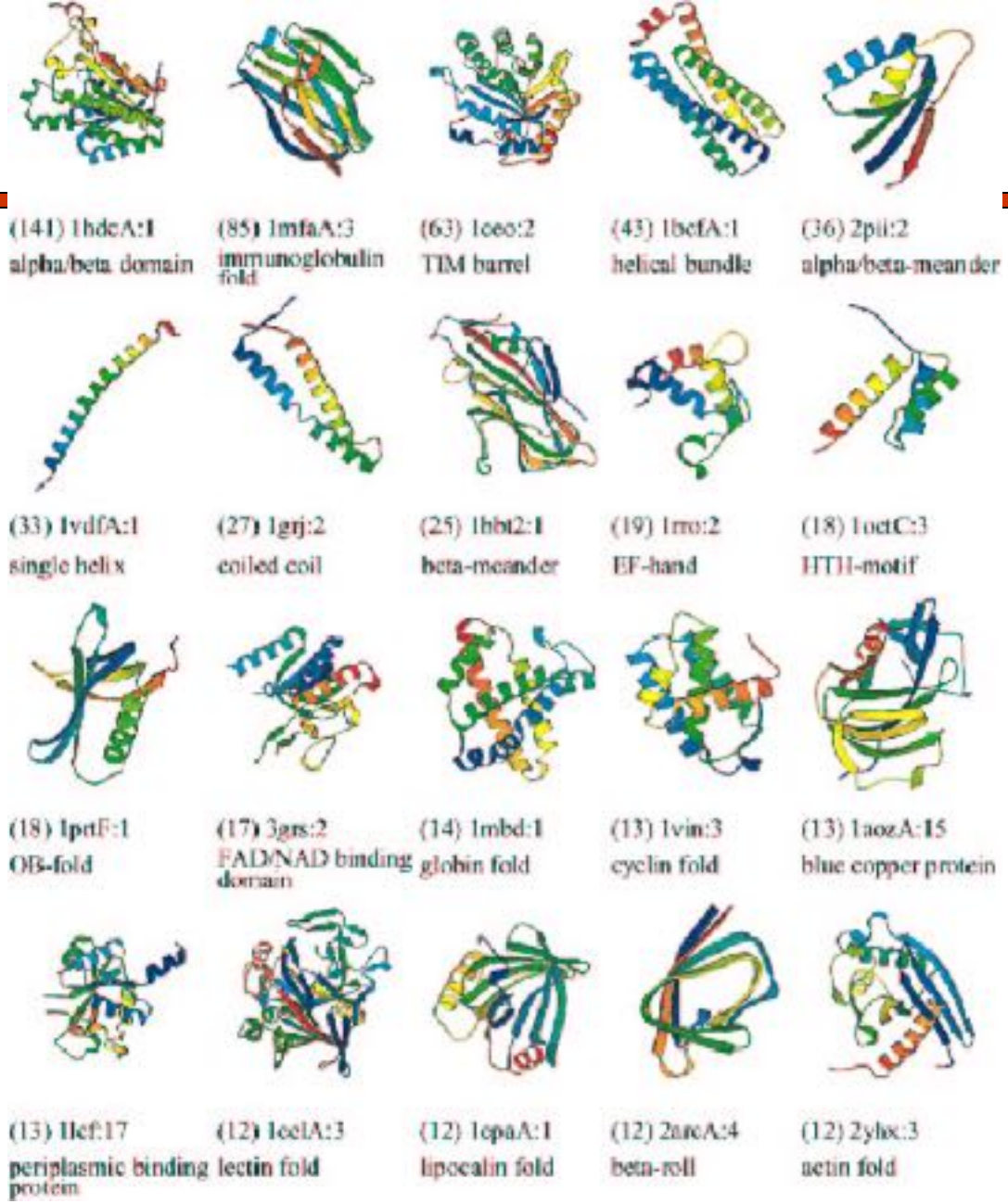


Structural neighbours of 1urnA (top left). 1mli (bottom right) has the same topology even though there are shifts in the relative orientation of secondary structure elements.

Sequence Alignment of Fold Neighbors



Frequent Fold Types



Protein Structure Prediction

- Holy Grail of bioinformatics
- Protein Structure Initiative to determine a set of protein structures that span protein structure space sufficiently well. WHY?
  - Number of folds in natural proteins is limited. Thus a newly discovered proteins should be within modeling distance of some protein in set.
- CASP: Critical Assessment of techniques for structure prediction
  - To stimulate work in this difficult field

PSP Methods

- homology-based modeling
- methods based on fold recognition
  - Threading methods
- ab initio methods
  - From first principles
  - With the help of databases

ROSETTA

- Best method for PSP
- As proteins fold, a large number of partially folded, low-energy conformations are formed, and that local structures combine to form more global structures with minimum energy.
- Build a database of known structures (I-sites) of short sequences (3-15 residues).
- Monte Carlo simulation assembling possible substructures and computing energy

Threading Methods

- See p471, Mount
  - **http://www.bioinformaticsonline.org/links/ch_10_t_7.html**

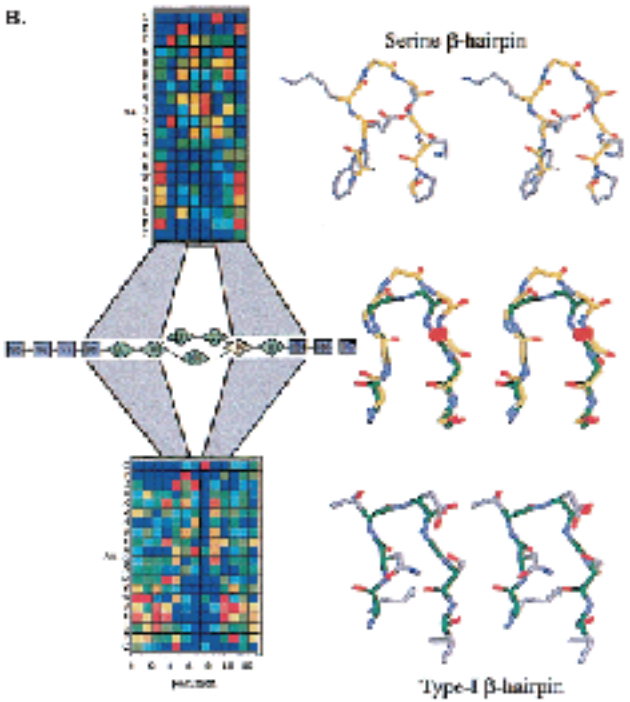


FIGURE 10.30. A hidden Markov model (discrete state-space model) of protein three-dimensional structure. (*B*) HMM called HMMSTR based on I sites, 3 to 15 amino acid patterns that are associated with three dimensional structural features. The two matrices with colored squares represent alignment of sets of patterns that are found to be associated with a structure, in this case the hairpin turns shown on the right. Each column in the table corresponds to the amino acid variation found for one structural position in one of the turns (*Blue* side chains) Conserved nonpolar residues; (*green*) conserved polar residues; (*red*) conserved prolines and (*orange*) conserved glycine. The two hairpins are aligned structurally in the middle structure on the right and the observed variation in the corresponding amino acid position is represented by the HMM between the matrices on the left. The HMM represents an alignment of the two hairpin structural motifs in three-dimensional space and an alignment of the sequences. A short mismatch in the turn is represented by splitting the model into two branches. The shaped icons represent states, each of which represents a structure and a sequence position. Each state contains probability distributions about the sequence and structural attributes of a single position in the motif, including the probability of observing a particular amino acid, secondary structure, Φ-Ψ backbone angles, and structural context, e.g., location of β strand in a β sheet. Rectangles are predominantly β-strand states, and diamonds are predominantly turns. The color of the icon indicates a sequence preference as follows: (*blue*) hydrophobic; (*green*) polar; and (*yellow*) glycine. Numbers in icons are arbitrary identification numbers for the HMM states. There is a transition probability of moving from each state in the model to the next, as in HMMs that represent msa's. This model is a small component of the main HMMSTR model that represents a merging of the entire I-sites library. Three different models, designated X', X", and X''', are included in HMMSTR, which differ in details as to how the alignment of the I-sites was obtained to design the branching patterns (topology) of the model and which structural data were used to train the model. HMMSTR may be used for a variety of different predictions, including secondary structure prediction, structural context prediction, and Φ Ψ dihedral angle prediction. Predictions are made by aligning the model with a sequence, finding if there is a high scoring alignment, and deciphering the highest scoring path through the model. The HMMSTR program may be downloaded or used on a server that can be readily located by a Web search. (*B*, reprinted, with permission, from Bystroff et al. 2000 [©2000 Elsevier].)

Modeling Servers

- SwissMODEL
- 3DJigsaw
- CPHModel
- ESyPred3D
- Geno3D
- SDSC1
- Rosetta
- MolIDE
- SCWRL
- PSIPred
- MODELLER
- LOOPY

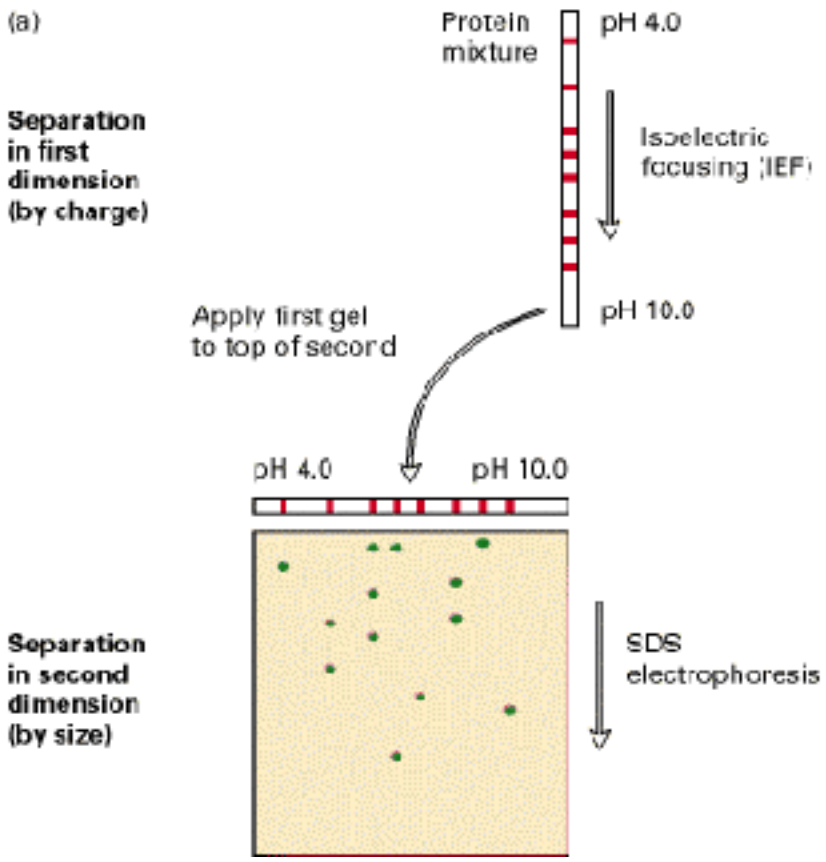
Genomics

- Study of all genes in a genome
  - All aspects of total gene content
  - Gene Expression
    - Microarray experiments & analysis
    - RNA-Seq

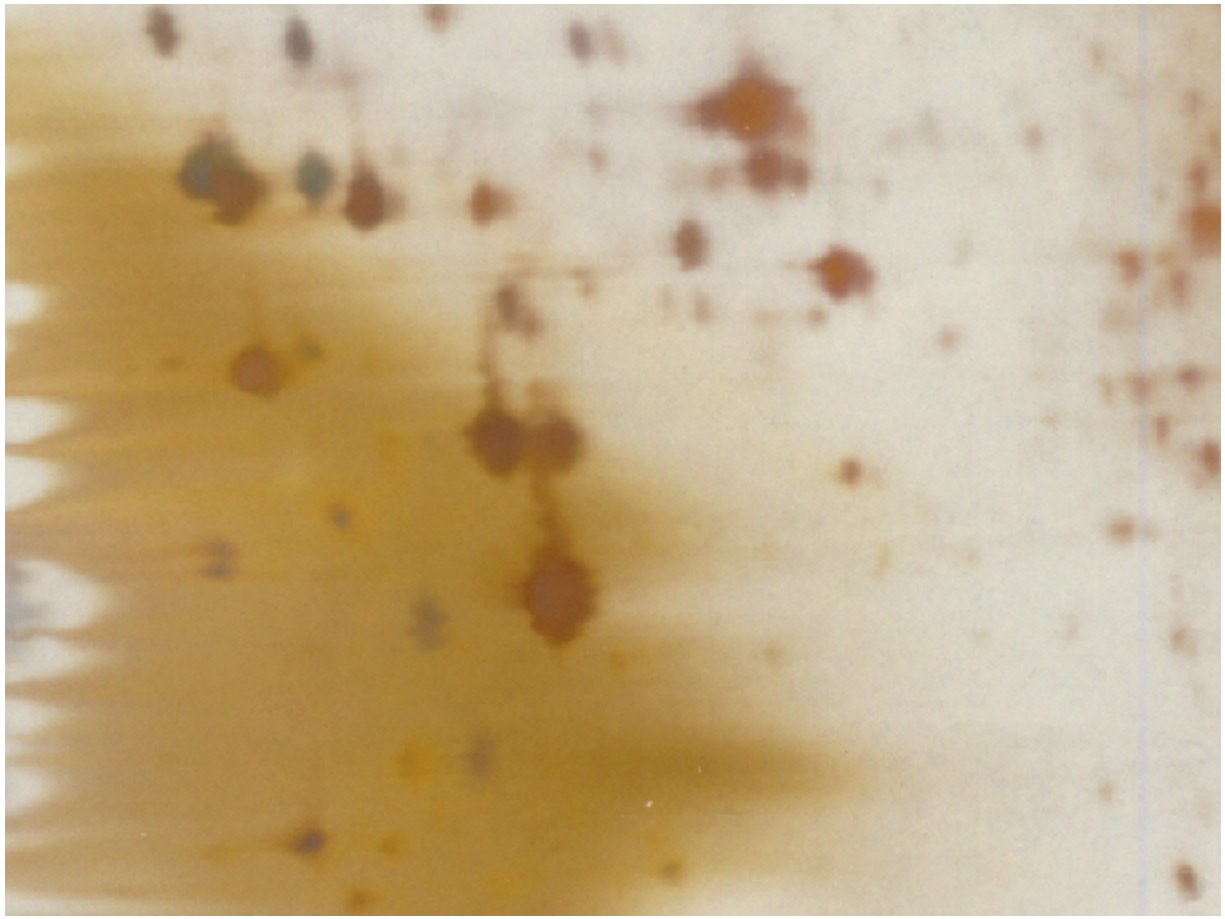
Proteomics

- Study of all proteins in a genome, or comparison of whole genomes.
  - Whole genome annotation & Functional proteomics
  - Whole genome comparison
  - Protein Expression: 2D Gel Electrophoresis

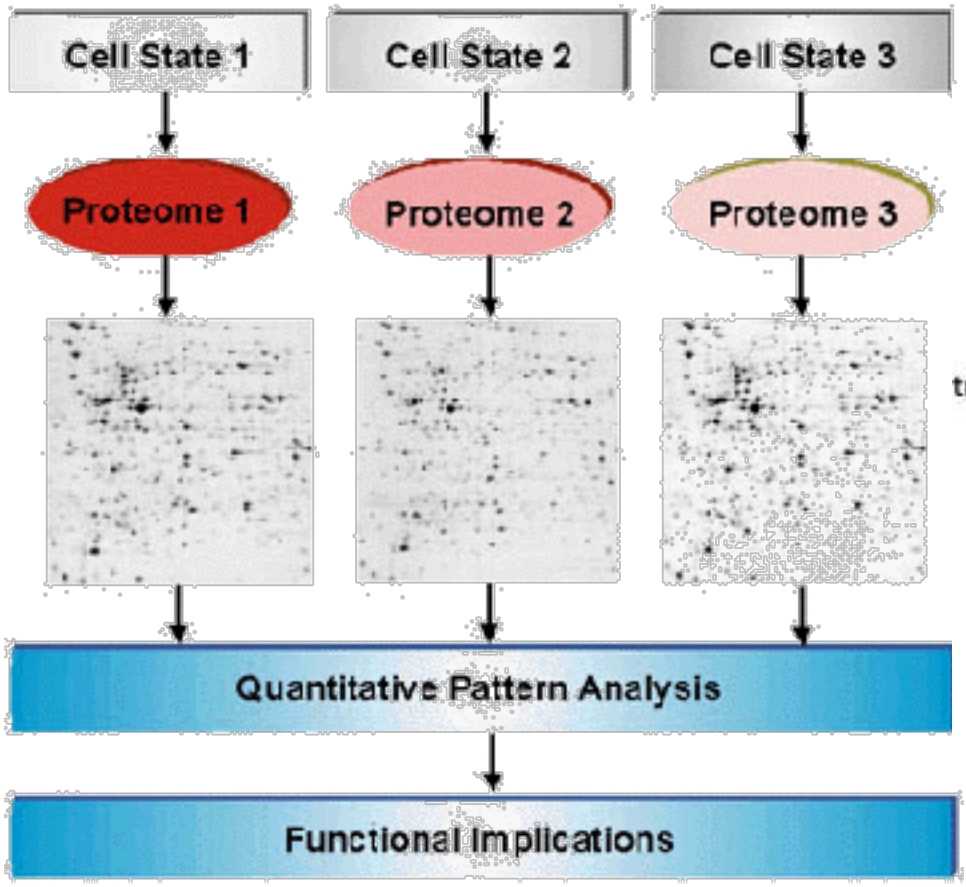
2D-Gels

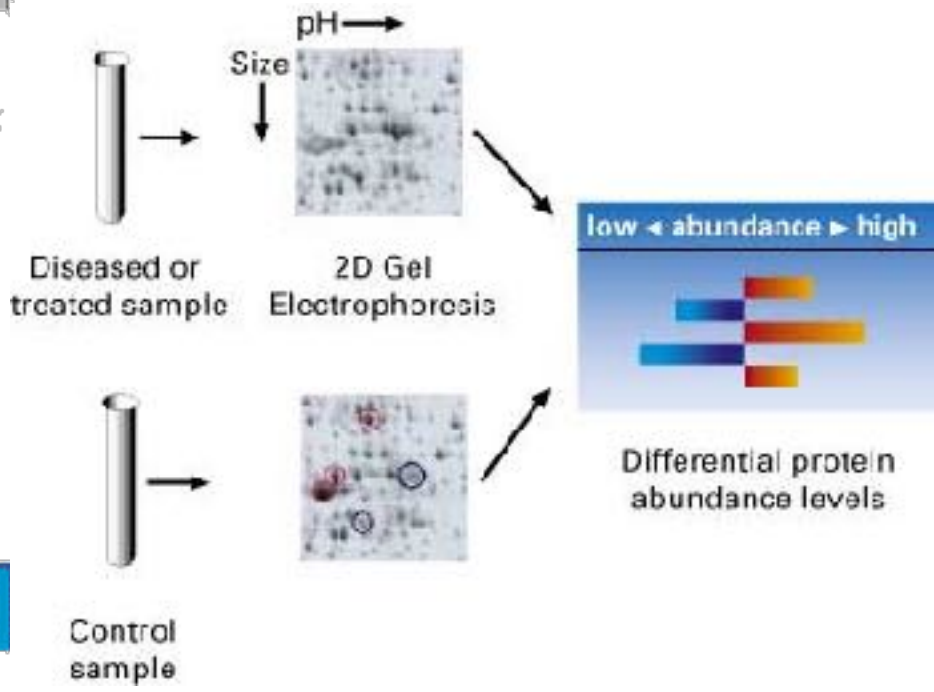

(a)
Protein mixture
pH 4.0
Separation in first dimension (by charge)
Isoelectric focusing (IEF)
pH 10.0
Apply first gel to top of second
pH 4.0
pH 10.0
Separation in second dimension (by size)
SDS electrophoresis

2D Gel Electrophoresis



2D-gels

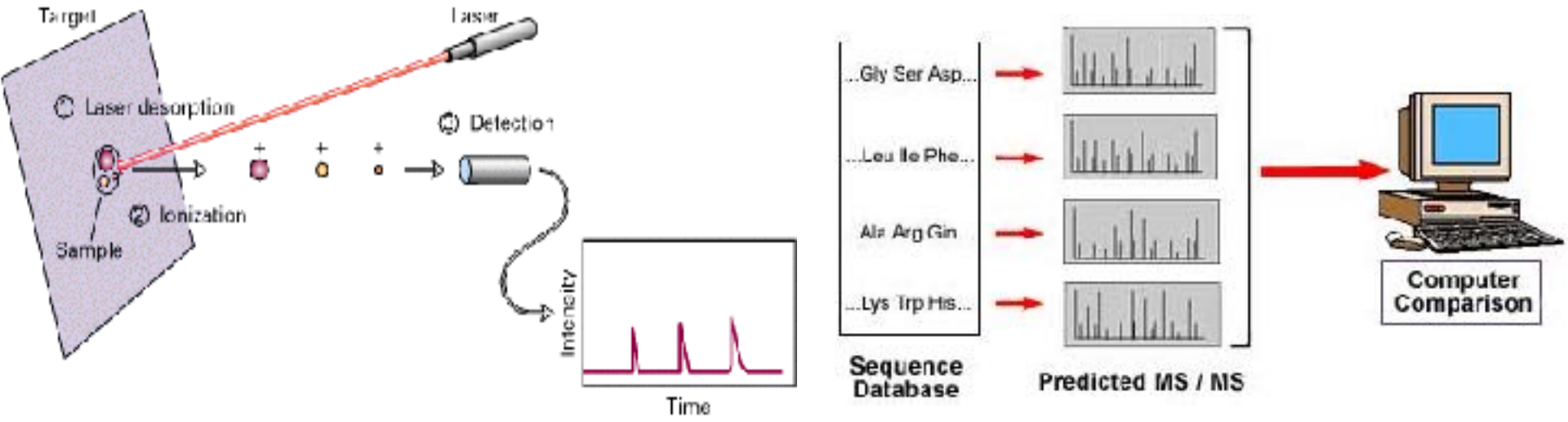




Comparing Proteomes For Differences in Protein Expression

Comparing Different Sample Types For Changes in Protein Levels

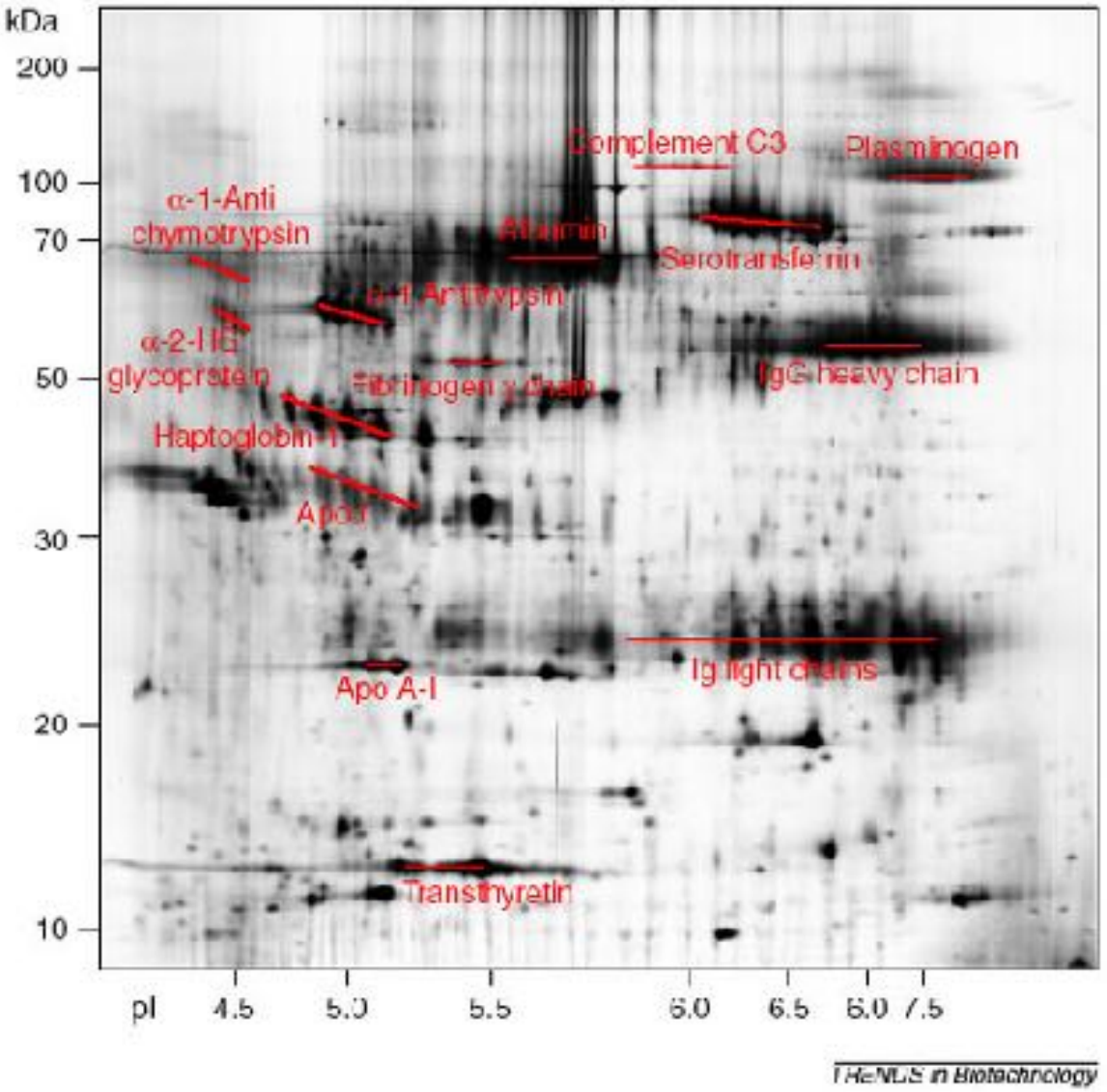
Mass Spectrometry



- **Mass measurements By Time-of-Flight**
  - Laser ionizes protein
  - Electric field accelerates molecules in sample toward detector
  - Time to detector is inversely proportional to mass of molecule
  - Infer molecular weights of proteins and peptides

Mass Spectrometry (MS)

- **Using Peptide Masses to Identify Proteins**
  - Peptide mass fingerprint is a compilation of molecular weights of peptides
  - Use molecular weight of native protein and MS signature to search database for similarly-sized proteins with similar MS maps
  - Fairly easy to sequence proteins using MS


kDa
200
100
70
50
30
20
10
pI
4.5
5.0
5.5
6.0
6.5
6.0
7.5
Complement C3
Plasminogen
α-1-Anti chymotrypsin
Albumin
Serotransferrin
α-1-Antitrypsin
α-2-HS glycoprotein
Fibrinogen γ chain
IgG heavy chain
Haptoglobin-1
Apo J
Apo A-I
Ig light chains
Transthyretin
TRENDS in Biotechnology

Other Proteomics Tools

From ExPASy/SWISS-PROT:

- **AACompIdent** identify proteins from aa composition

[Input: aa composition, isoelectric point, mol wt., etc. Output: proteins from DB]

- **AACompSim** compares proteins aa composition with other proteins
- **MultIdent** uses mol wt., mass fingerprints, etc. to identify proteins
- **PeptIdent** compares experimentally determined mass fingerprints with theoretically determined ones for all proteins
- **FindMod** predicts post-translational modifications based on mass difference between experimental and theoretical mass fingerprints.
- **PeptideMass** theoretical mass fingerprint for a given protein.
- **GlycoMod** predicts oligosaccharide modifications from mass difference
- **TGREASE** calculates hydrophobicity of protein along its length