## **Protein Representations**



human chorionic gonadotropin (hCG, from PDB ID 1HCN)

#### **Types of Proteins**

Secondary structure	Φ	Ψ	Rise per residue
α-helix	$-57^{\circ}$	$-47^{\circ}$	1.5 Å (3.6 residues per turn)
Coiled-coil	$-64^{\circ}$	$-42^{\circ}$	1.5 Å
$\beta$ -sheet (antiparallel)	-139°	$135^{\circ}$	$3.5\mathrm{\AA}$
β-sheet (parallel)	-119°	113°	$3.5\mathrm{\AA}$
Collagen	$-51^{\circ}$	153°	3 Å

**1. Fibrous proteins** Coiled-coil

Coiled-coil protein (from PDB ID 3Q0X)



Model collagen peptide (from PDB ID 3ADM)

### 2. Membrane proteins



Cytochrome c oxidase (from PDB ID 2OCC)

### 3. Globular proteins



Myoglobin (PDB ID 1A6M)

# **Protein Folding**

Forces

1.

- 2.
- 3.
- 4.
- 5.

Optimum distances between nuclei (Å)

Optimum distances between nuclei (A)								
Atom	С	Ν	0	Н				
С	3.2	2.9	2.8	2.4	ß			
Ν		2.7	2.7	2.4	nerg			
0			2.7	2.4	E	ro		
Н				2.0	0	Distance		
		$F = -\frac{A}{r^6} + \frac{A}{r}$	B 12			between atoms		

## Thermodynamics of Protein Folding

$Protein_{unfolded}$ — Protein <sub>folded</sub>					
Thermodynamic Parameter	Polar residues	Non-polar residues			
$\Delta H_{chain}$					
$\Delta H_{solvent}$					
$(-T\Delta S_{chain})$					
$(-T\Delta S_{solvent})$					
Overall ∆G					

## **Kinetics of Protein Folding**









Thermodynamic stability

Kinetic stability

## Chaperones

Heat Shock Proteins (hsp)

