FACTORS AFFECTING α-HELIX STABILITY

1. electrostatic repulsion/attraction between adjacent residues with charged R groups
2. bulkiness of adjacent R groups
3. interactions between residues spaced 3 or 4 residues apart (same side of helix)
4. occurrence of Pro residues ("kink" in backbone destabilizes helix, and amide N of Pro has no H for hydrogen bonding. Nevertheless, though it's rare, there ARE occasional Pro residues found in real proteins in α-helices.)
5. interaction between R groups at ends of helix and the dipole of the helix
   – charged R groups often near N-term. (δ+) end of helix (increases stability of helical structure)
   + charged R groups often near C-term. (δ –) end of helix (increases stability of helical structure)

COMPARISON OF α-HELIX AND β-CONFORMATION

Parameter	α-helix	β-conformation
number of backbone strands involved	1	at least 2; strands can be parallel or antiparallel
hydrogen bonding	intrachain; carbonyl O of residue n to amide N-H of residue (n + 4); H-bonds nearly parallel to helix axis (overall backbone "direction")	interchain or intrachain between different parts of chain; carbonyl O on one strand to amide N-H on another strand or on another part of same strand; H-bonds more or less perpendicular to backbones
repeat unit (don't memorize distances!)	one turn of helix (0.54 nm) (3.6 residues per turn)	2 amino acid residues (0.65 - 0.70 nm)
R groups	regular helical array pointing out from axis (can have noncovalent interactions between R groups on adjacent turns on same side of helix)	regular array with R groups alternating above and below plane of sheet
supersecondary structure (examples -- nature of stabilizing forces depends on specific protein) (This will be covered under fibrous proteins; it's not on Exam 1 9/17/01)	coiled coils with noncovalent bonds (van der Waals, hydrophobic, ionic, and/or hydrogen bonds) and sometimes also disulfide bonds between R groups on adjacent helices, e.g. in α-keratins	stacked sheets with van der Waals interactions between closedly packed R groups (in silk fibroin); in other proteins, can also have other noncovalent interactions between R groups, esp. hydrophobic interactions
other	helix as a whole has a dipole (δ^+ at N-terminal end and δ^- at C-terminal end)	