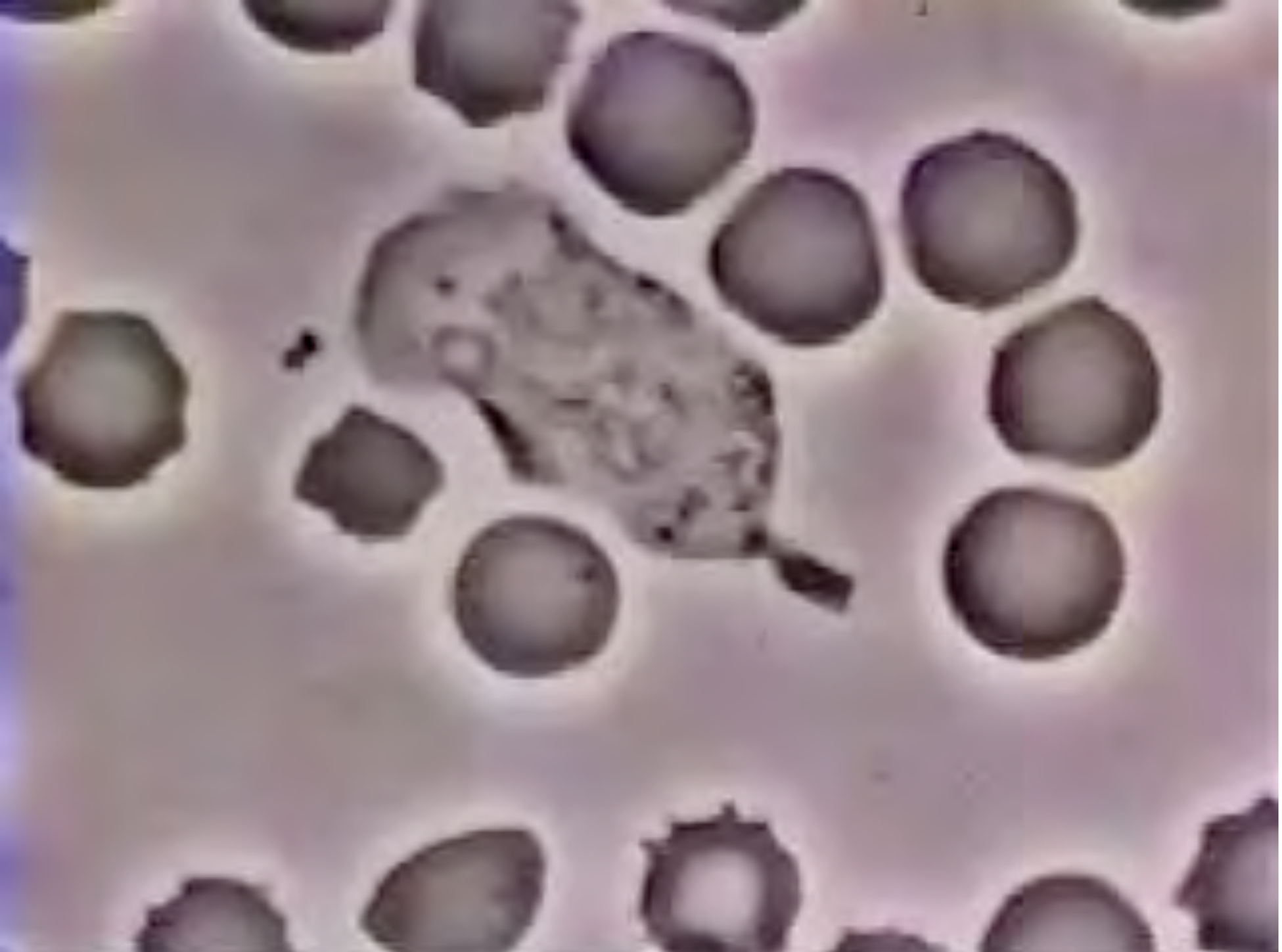


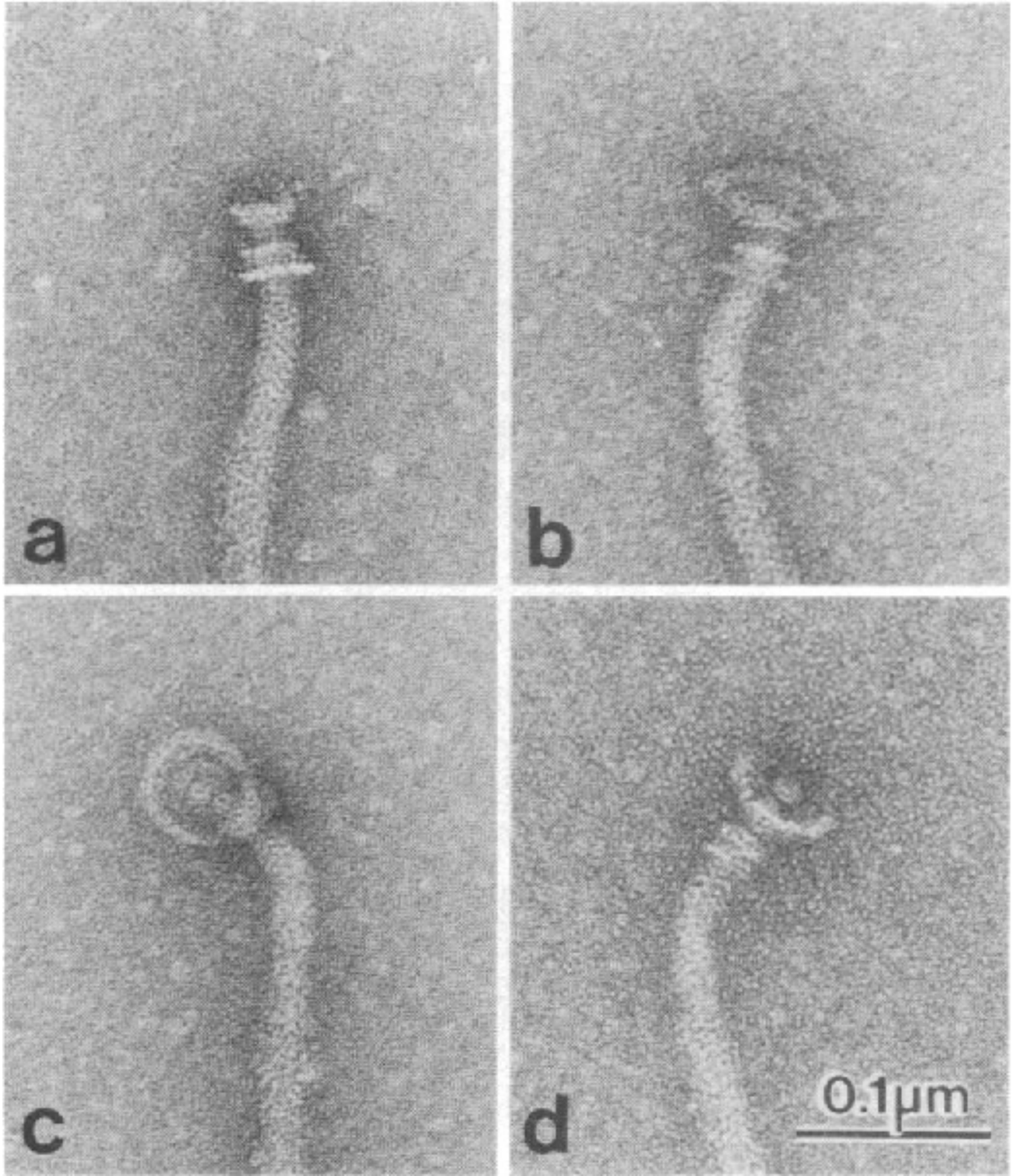
LECTURE 3

POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence



LECTURE 3

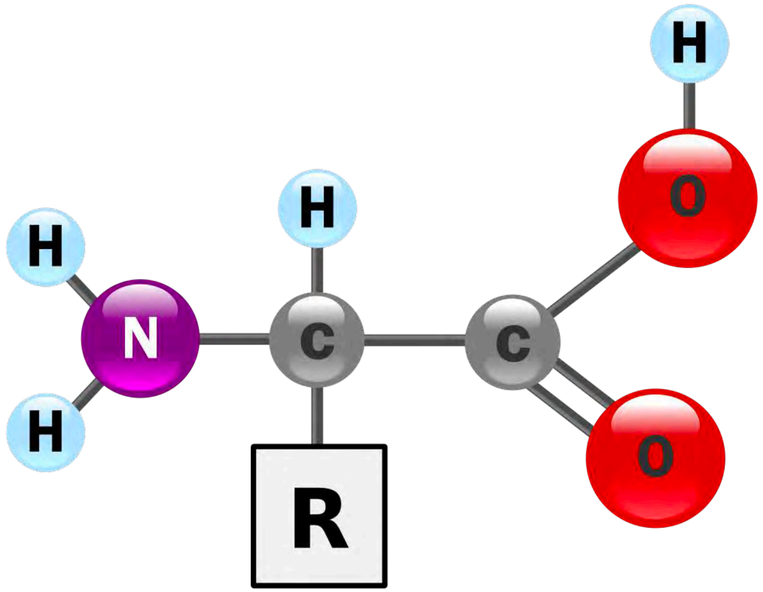
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

amino acid



20 different variants or this organic group in essential amino acids

LECTURE 3

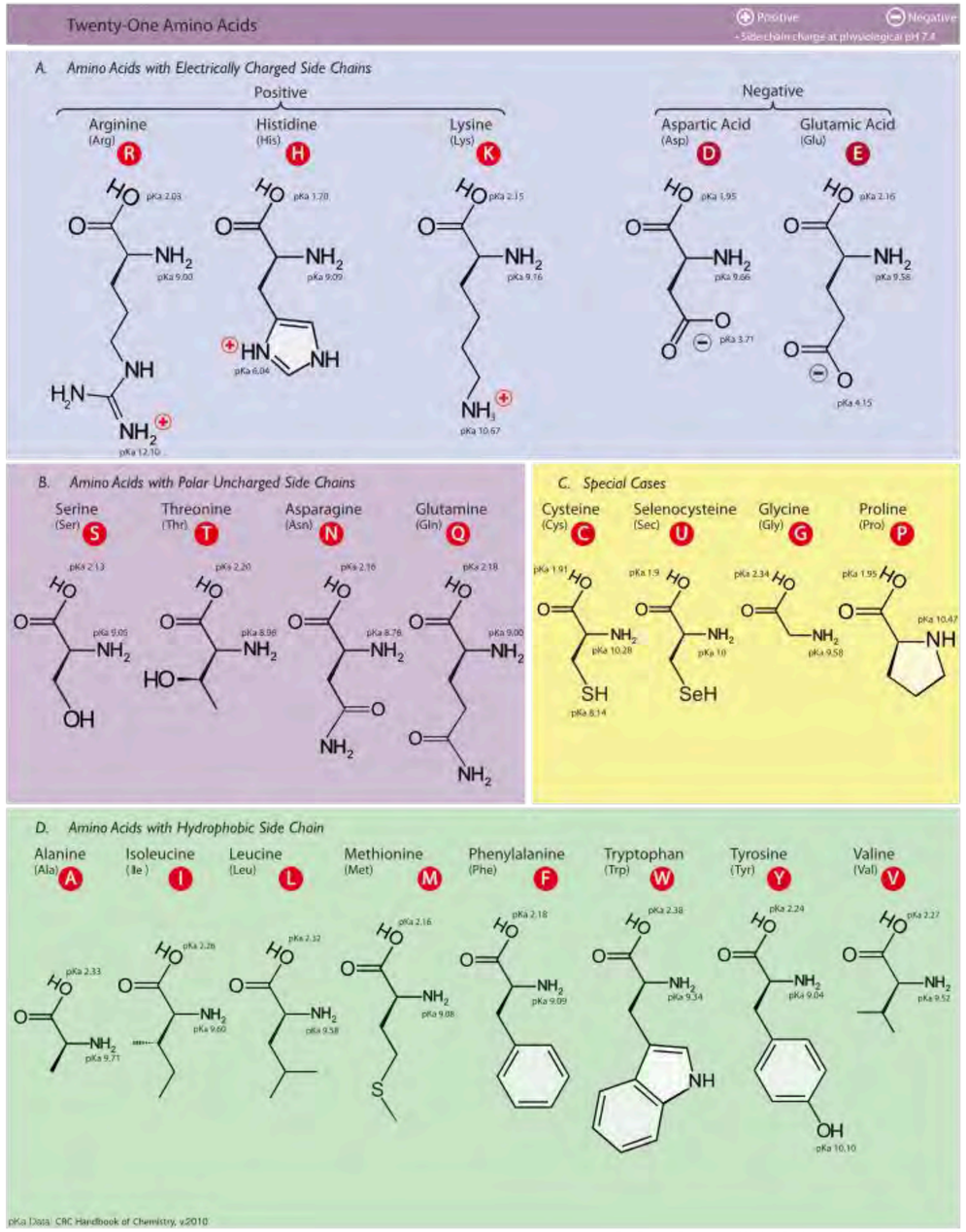
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

essential amino acids



LECTURE 3

POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

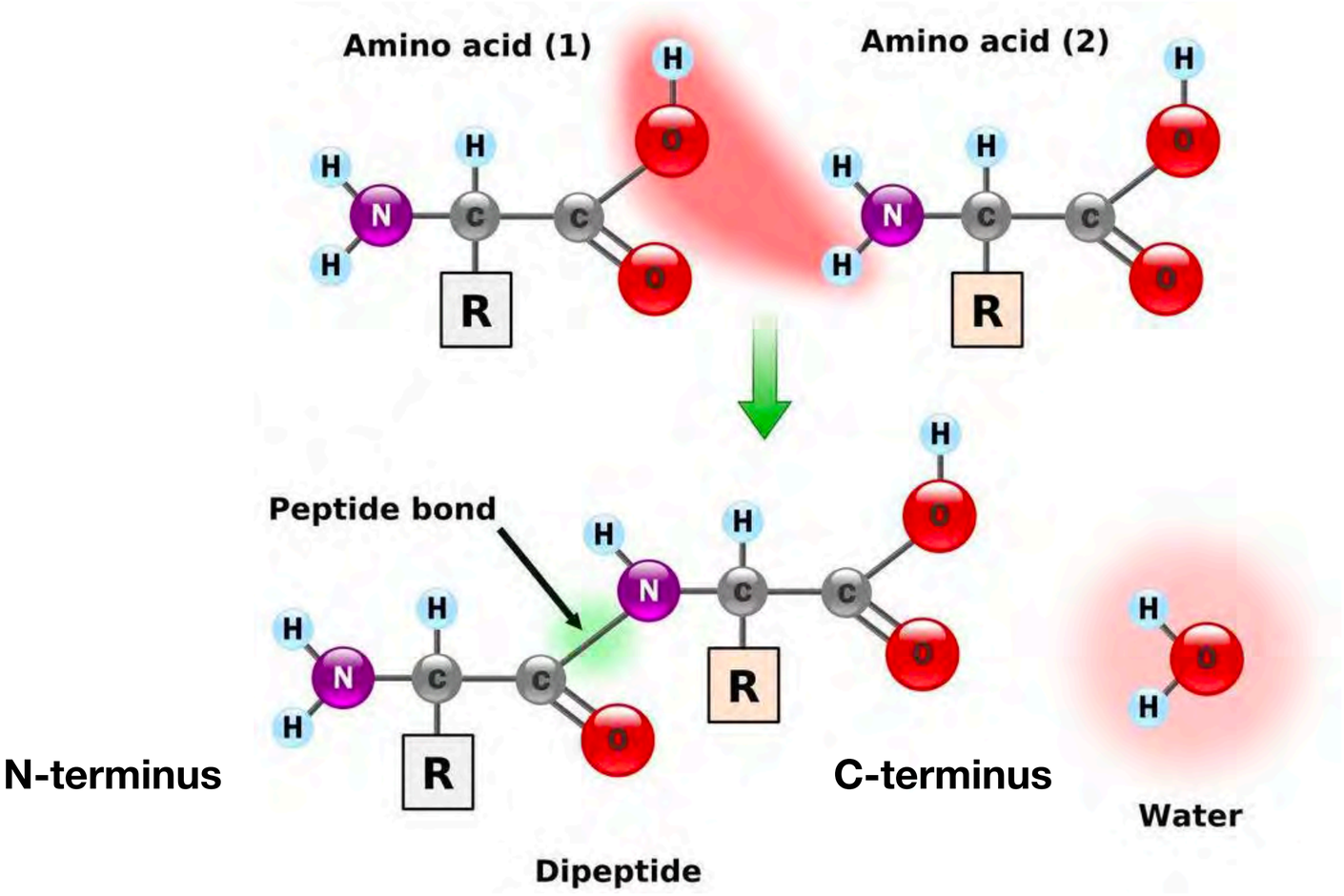
protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

peptide bond

LECTURE 3

POLYPEPTIDE **SYNTAX**

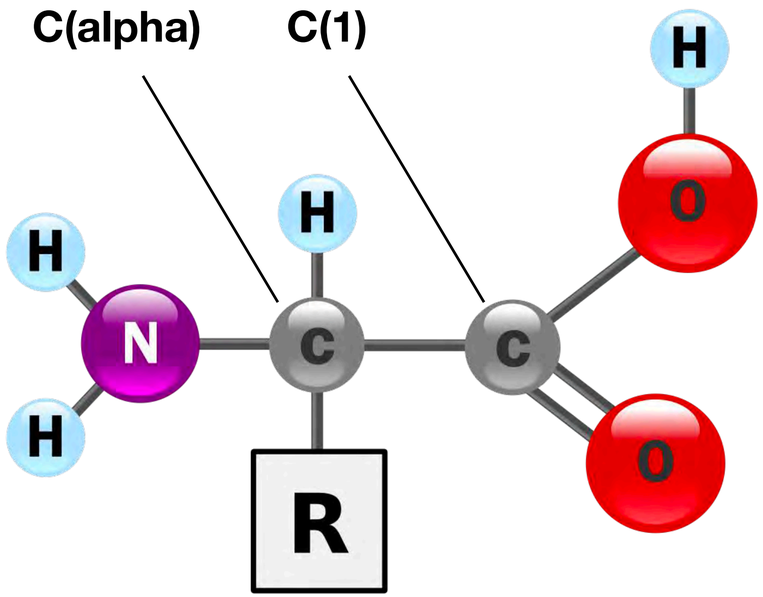


Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

polypeptide carbons



LECTURE 3

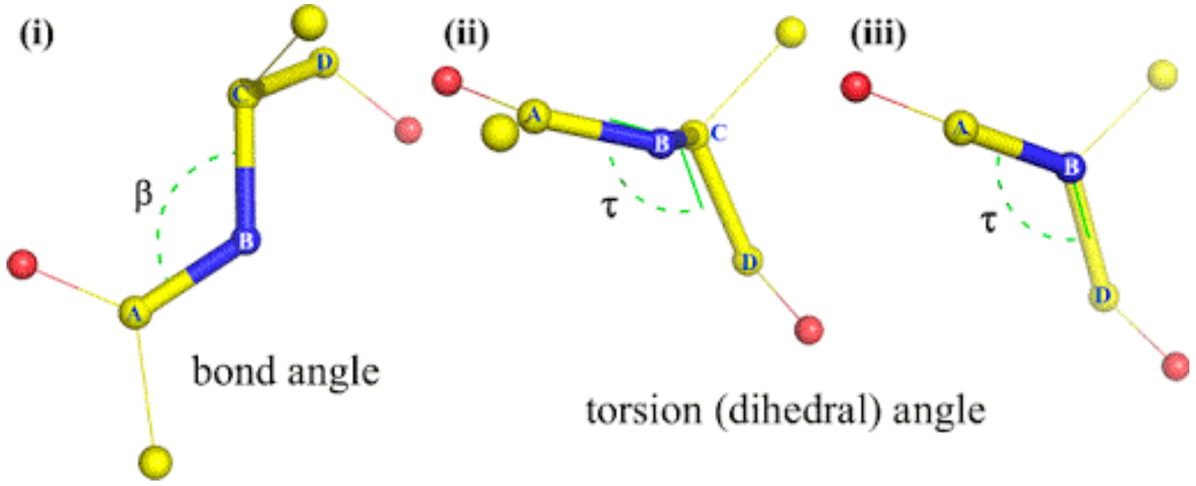
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

polypeptide angles



~constant **variable**

LECTURE 3

POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

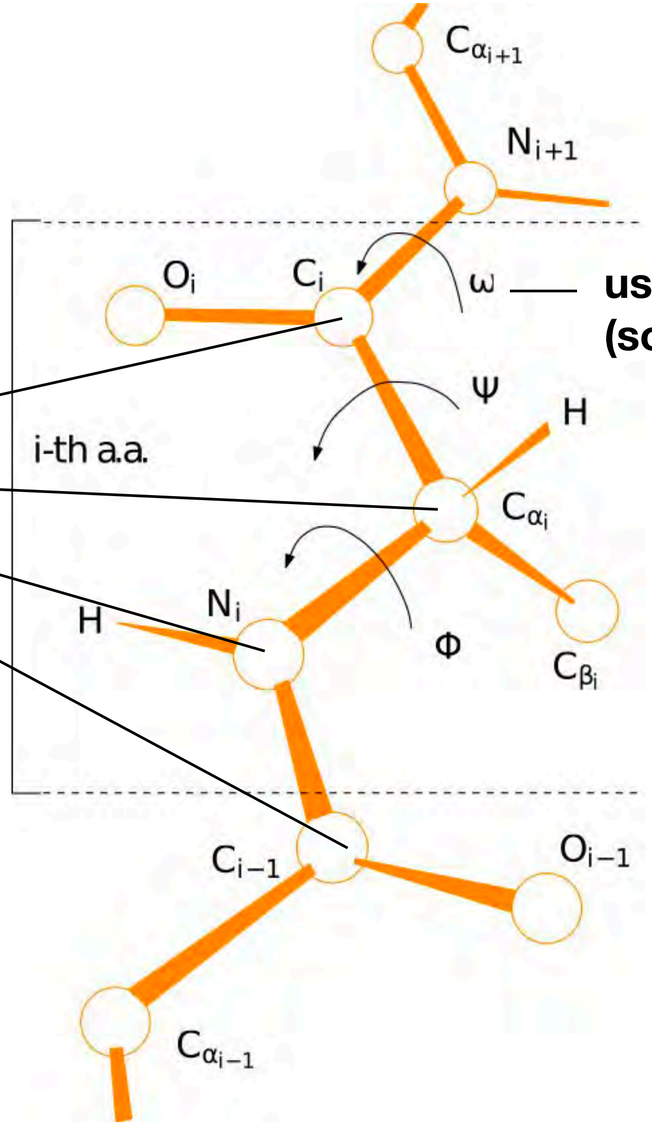
protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

LECTURE 3
POLYPEPTIDE **SYNTAX**

dihedral angles

four backbone atoms per each dihedral angle

atoms used to measure phi



usually 180deg (sometimes 0deg in proline)

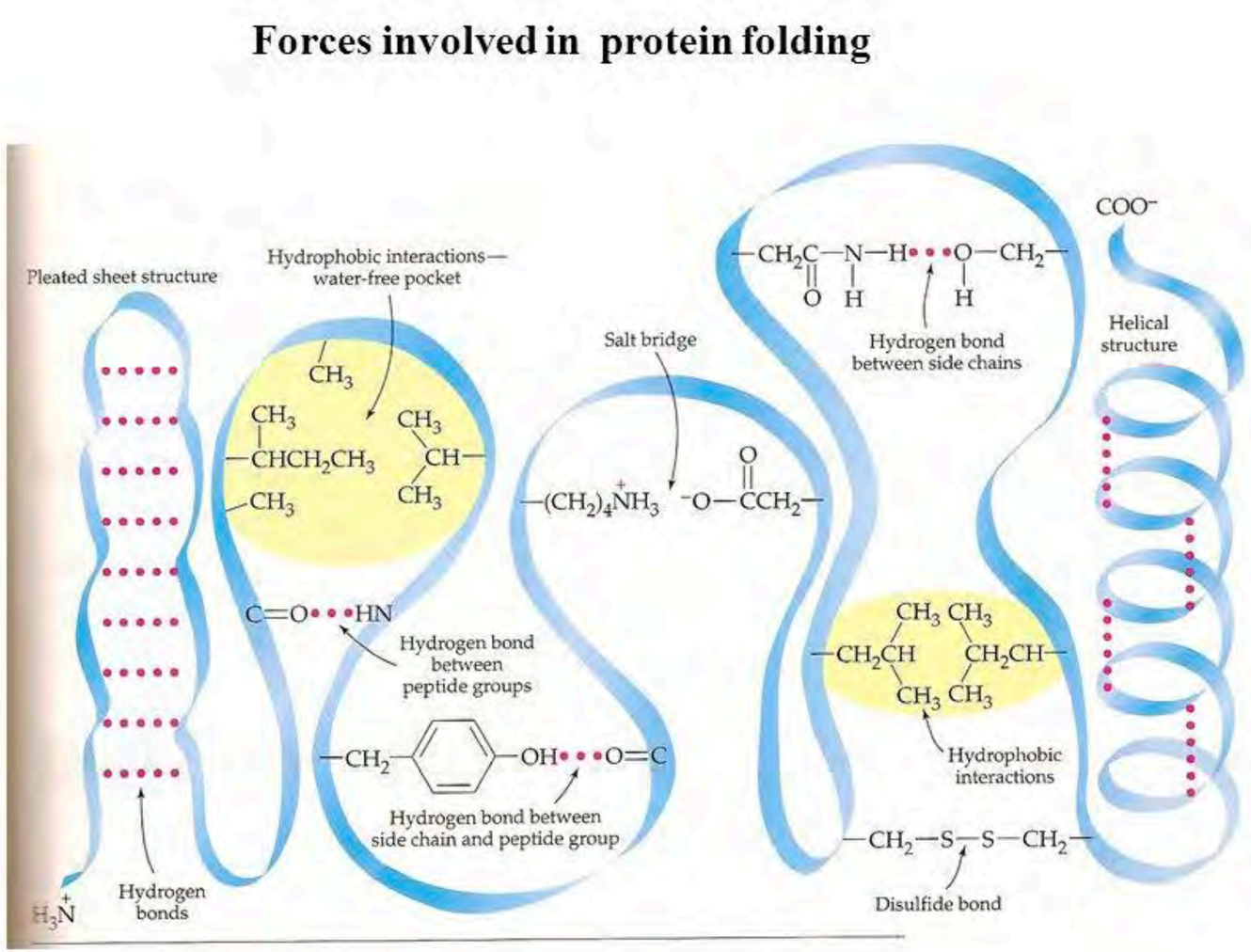
Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

protein folding

LECTURE 3
POLYPEPTIDE **SYNTAX**

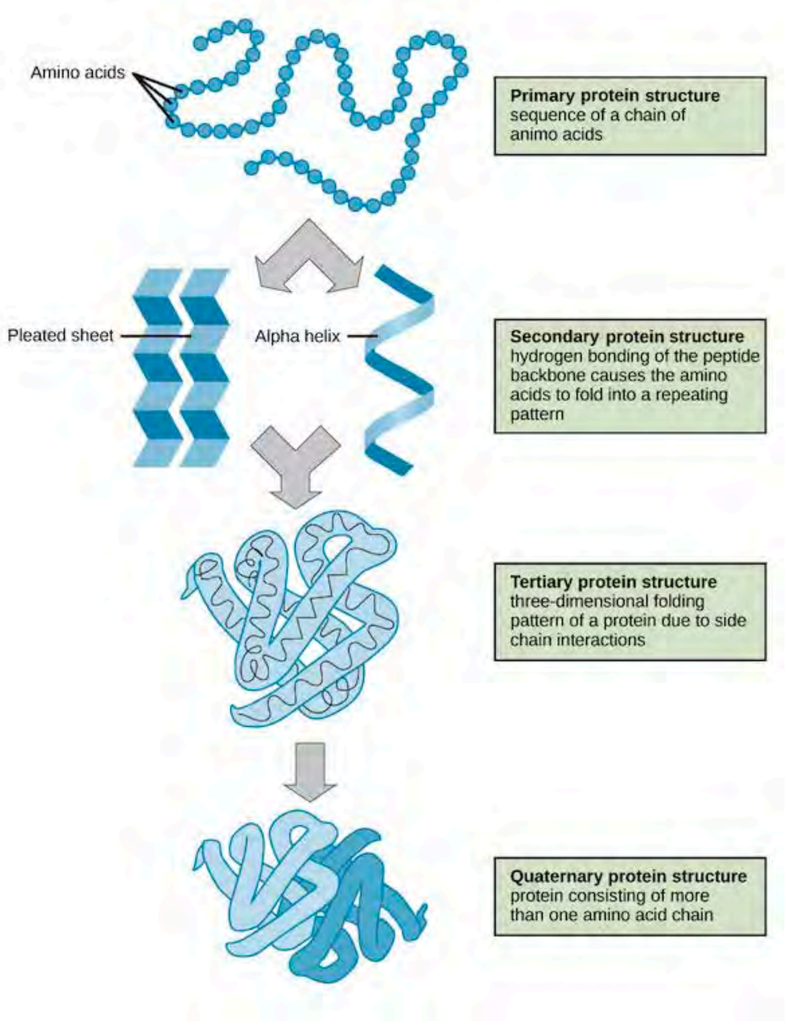


Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

protein folding



LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

alpha helix secondary structure

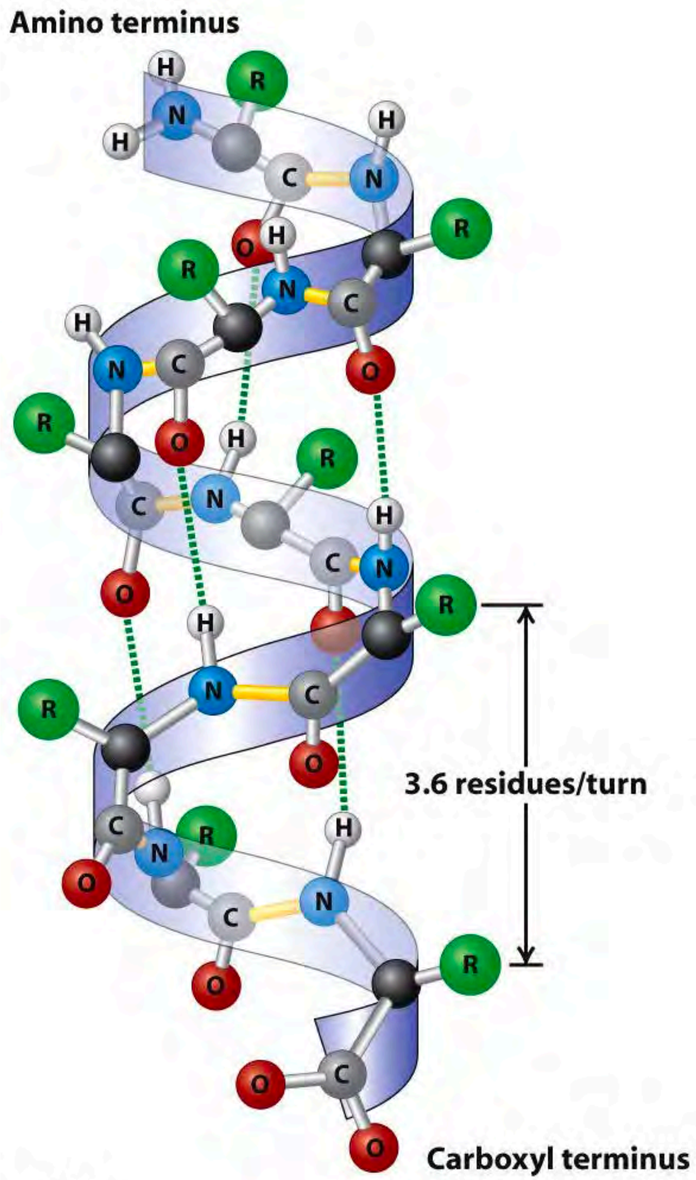


Figure 3-4
Molecular Cell Biology, Sixth Edition

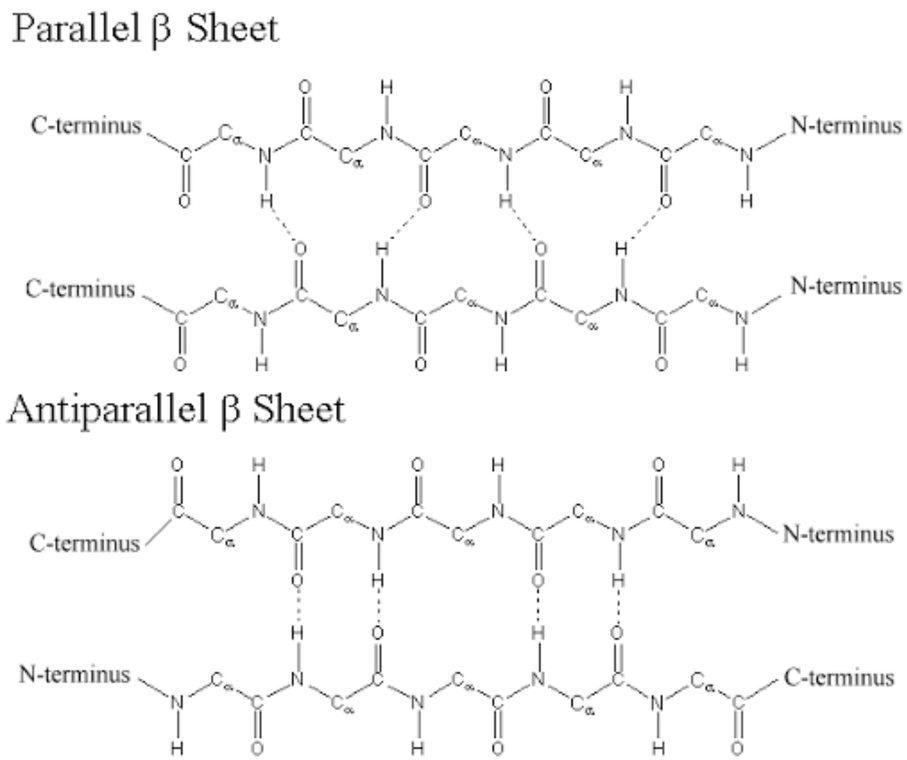
LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

beta sheet secondary structure



LECTURE 3

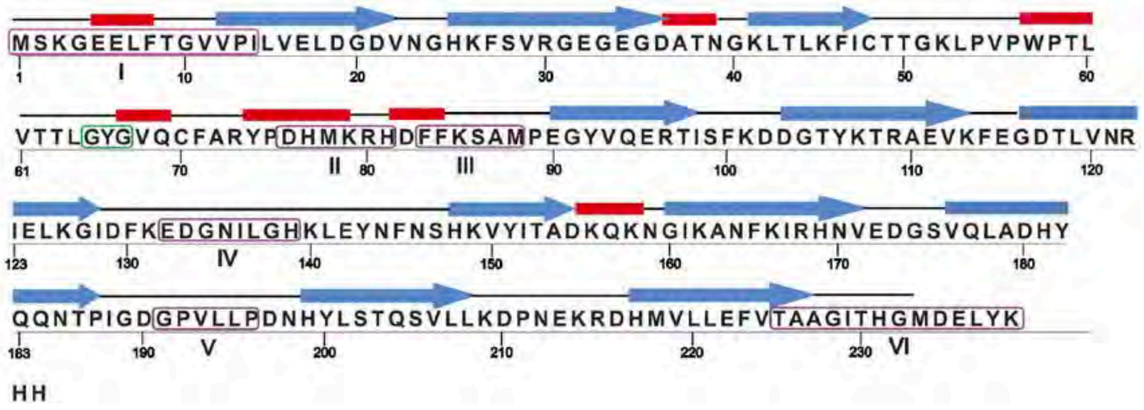
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

secondary structure annotation



LECTURE 3

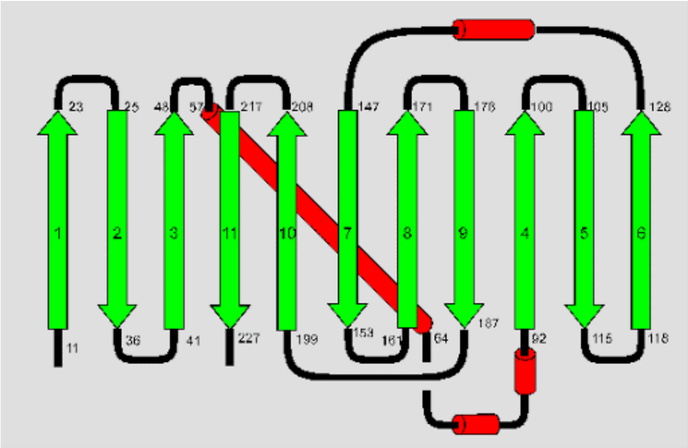
POLYPEPTIDE **SYNTAX**

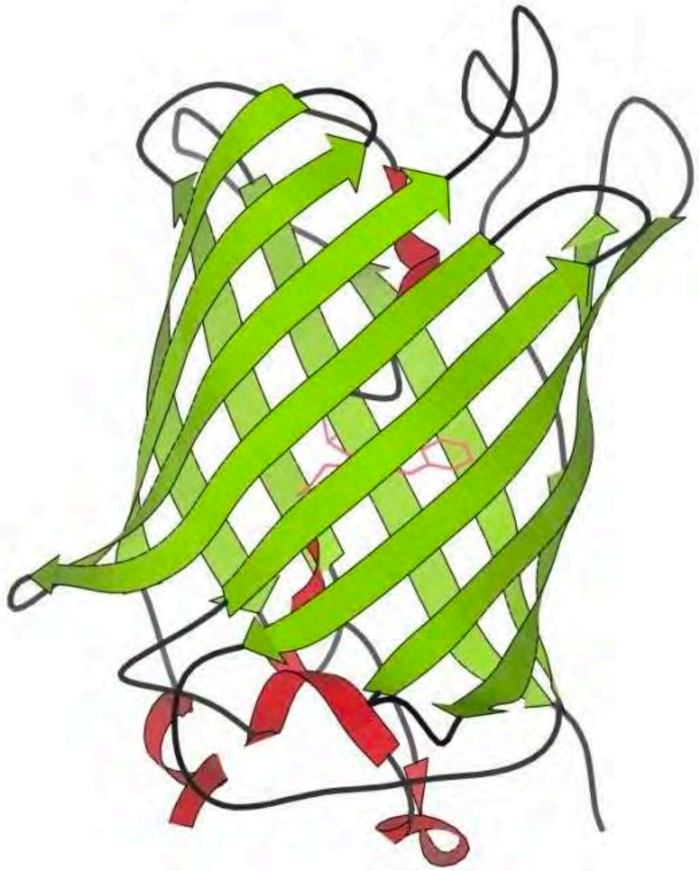
Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

ribbon representation
tertiary + secondary





LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

protein jewelry

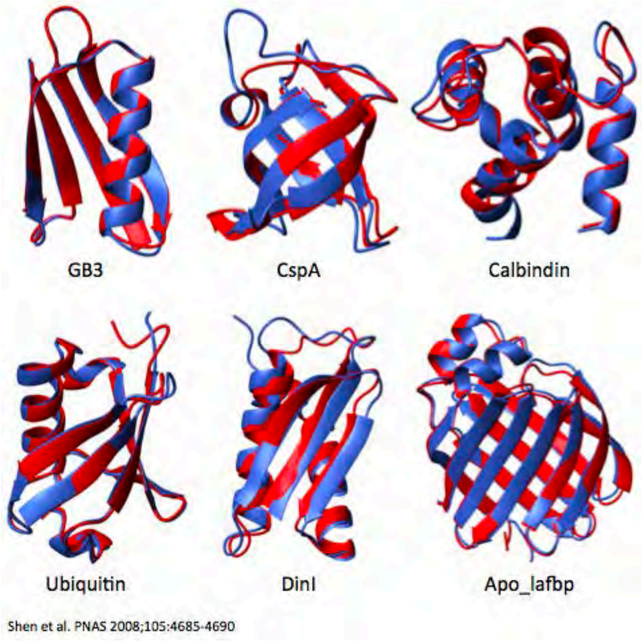
LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

tertiary structure
stochasticity



LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

molecular properties
molecular weight

LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

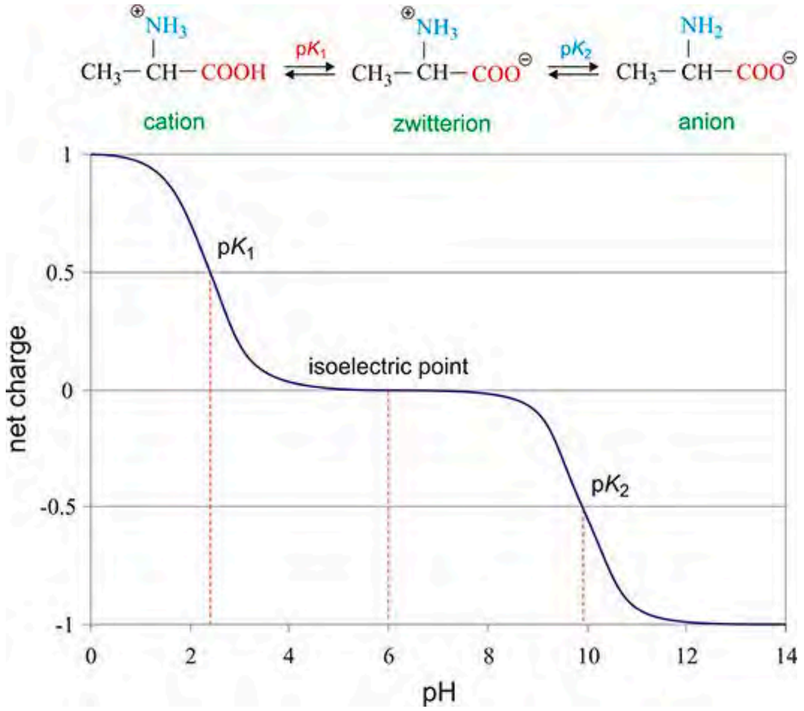
protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

Table 6–1 Molecular data on some proteins

	Molecular weight	Number of residues	Number of polypeptide chains
Insulin (bovine)	5,733	51	2
Cytochrome *c* (human)	13,000	104	1
Ribonuclease A (bovine pancreas)	13,700	124	1
Lysozyme (egg white)	13,930	129	1
Myoglobin (equine heart)	16,890	153	1
Chymotrypsin (bovine pancreas)	21,600	241	3
Chymotrypsinogen (bovine)	22,000	245	1
Hemoglobin (human)	64,500	574	4
Serum albumin (human)	68,500	~550	1
Hexokinase (yeast)	102,000	~800	2
Immunoglobulin G (human)	145,000	~1,320	4
RNA polymerase (*E. coli*)	450,000	~4,100	5
Apolipoprotein B (human)	513,000	4,536	1
Glutamate dehydrogenase (bovine liver)	1,000,000	~8,300	~40

molecular properties
isoelectric point



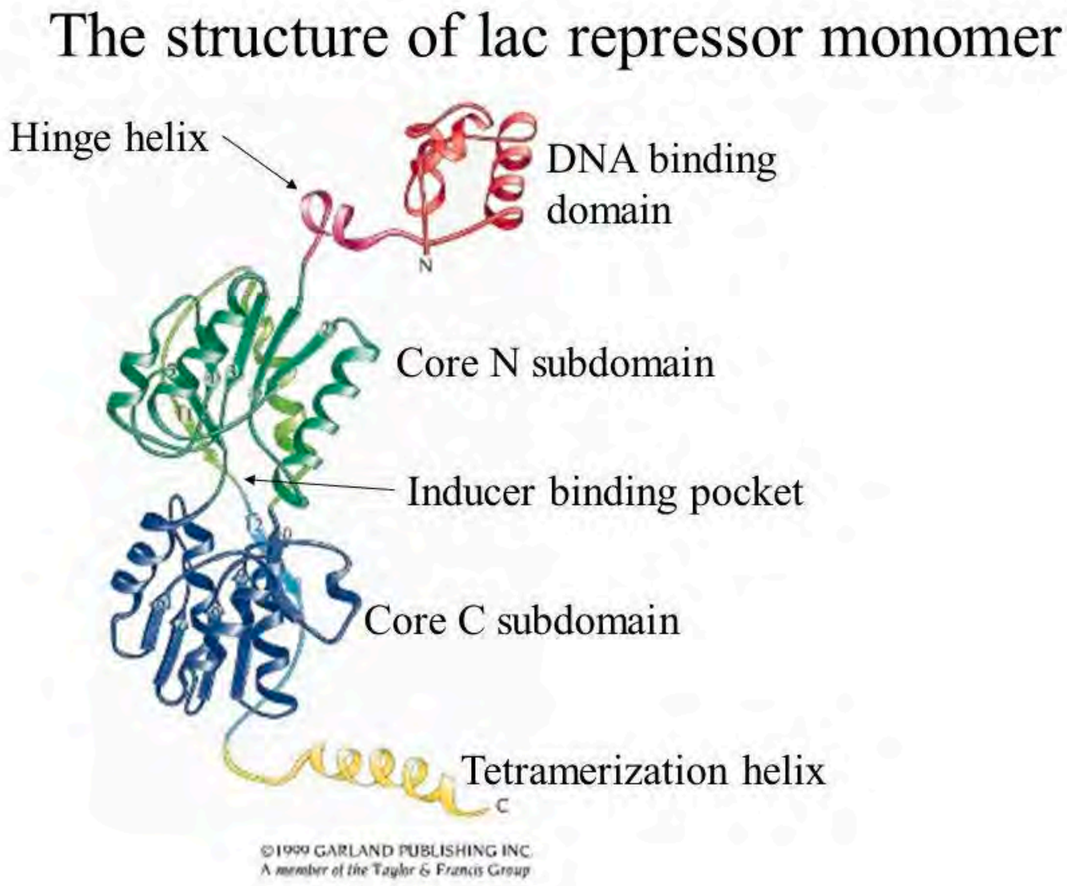
LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

protein domains



LECTURE 3

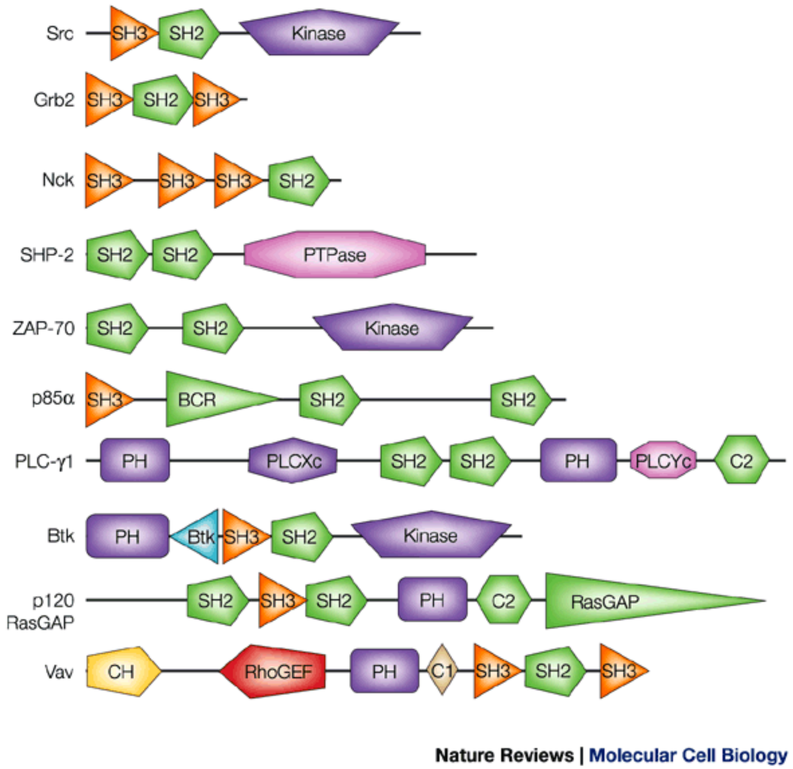
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

domain annotation



LECTURE 3

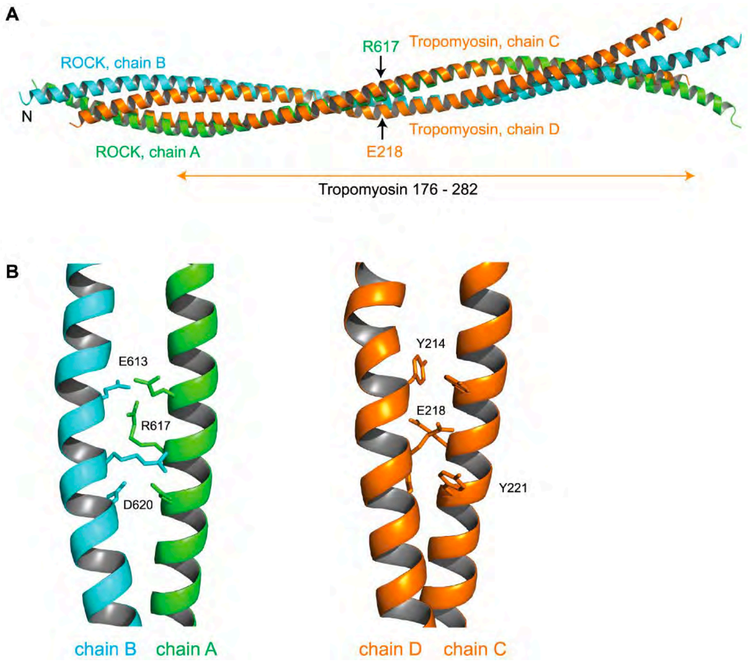
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

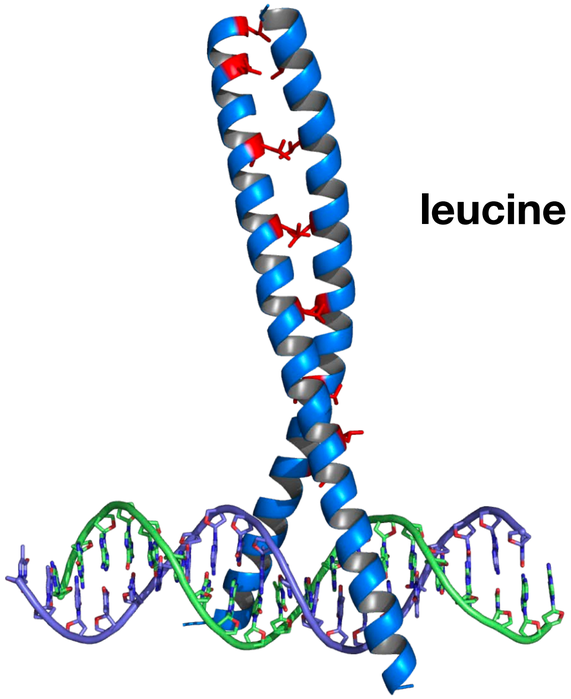
protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

binding domain



coiled coil domain



leucine zipper

LECTURE 3

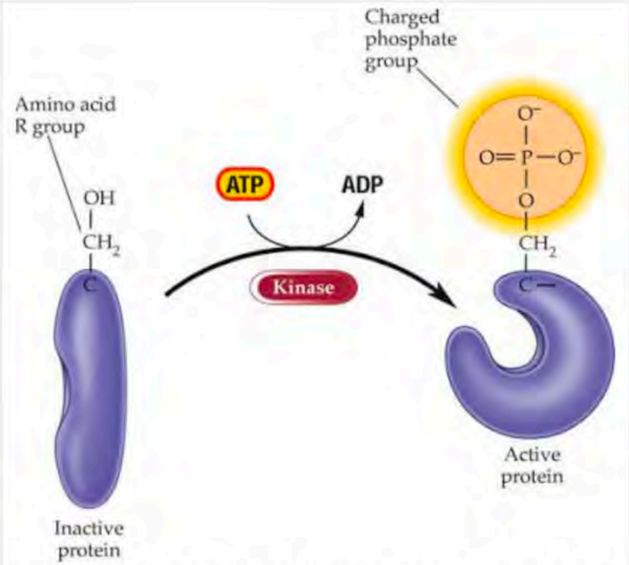
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

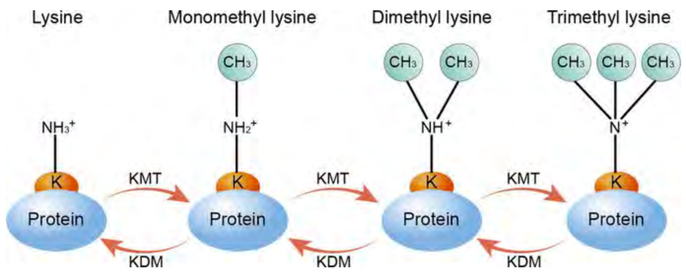
protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

post-translational modification
addition of small groups



Phosphorylation changes the shape of the protein (from Campbell's "Biology")

phosphorylation
Y/R/H/K/S/T



methylation
R/K/termini

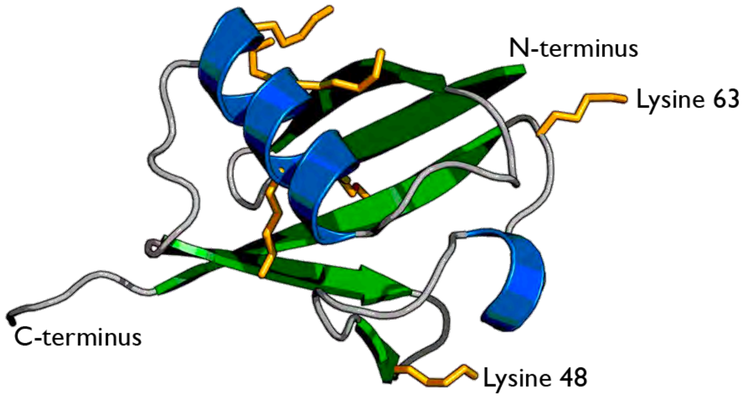
LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

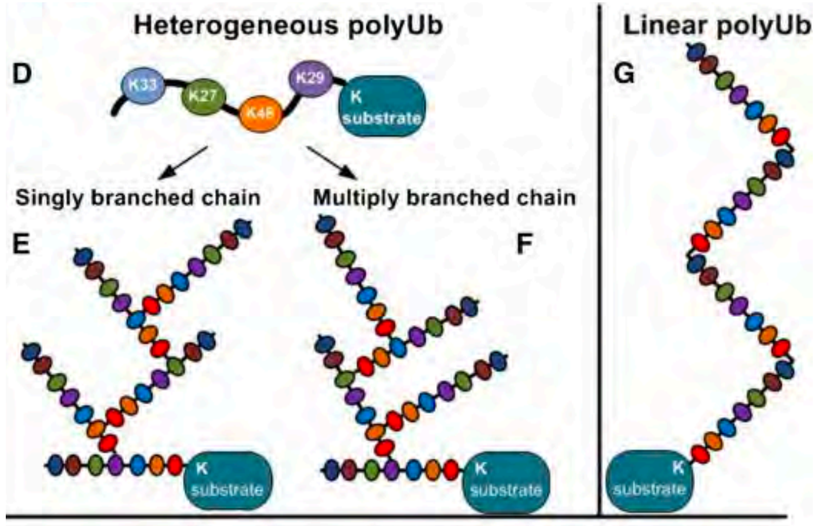
protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

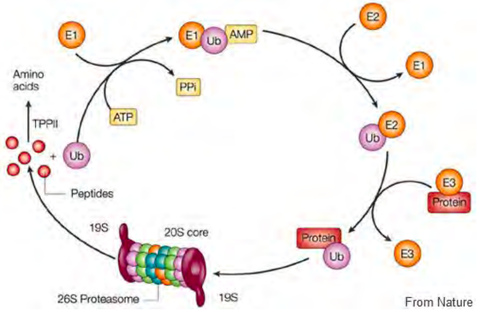
post-translational modification
addition of bigger groups



ubiquitin



ubiquitination
K



protein targeting
to proteasome

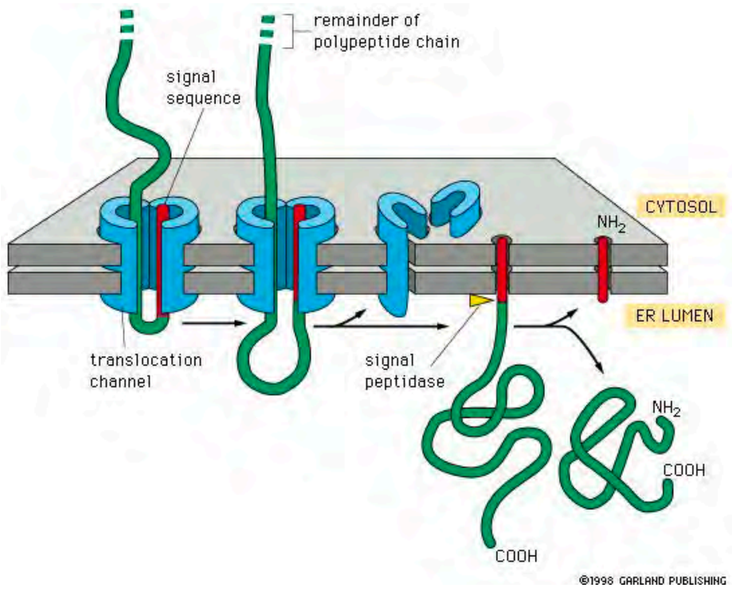
LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

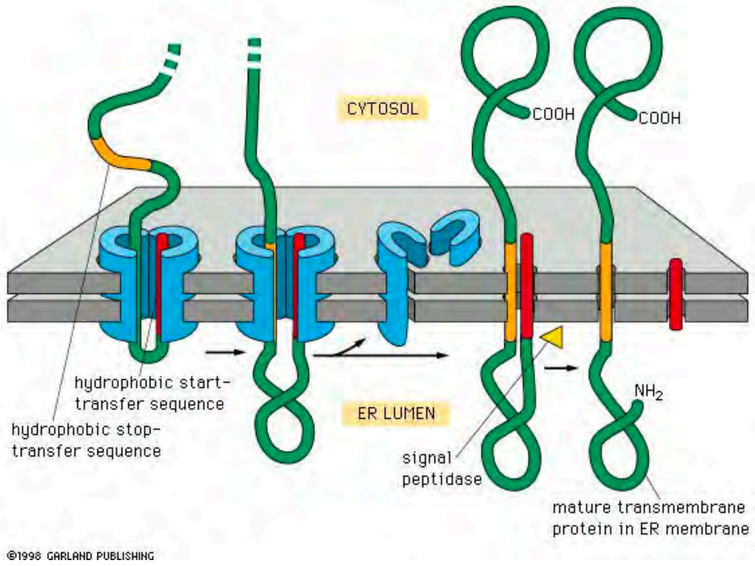
protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

targeting domains



protein targeting endoplasmic reticulum



protein targeting membrane proteins

LECTURE 3

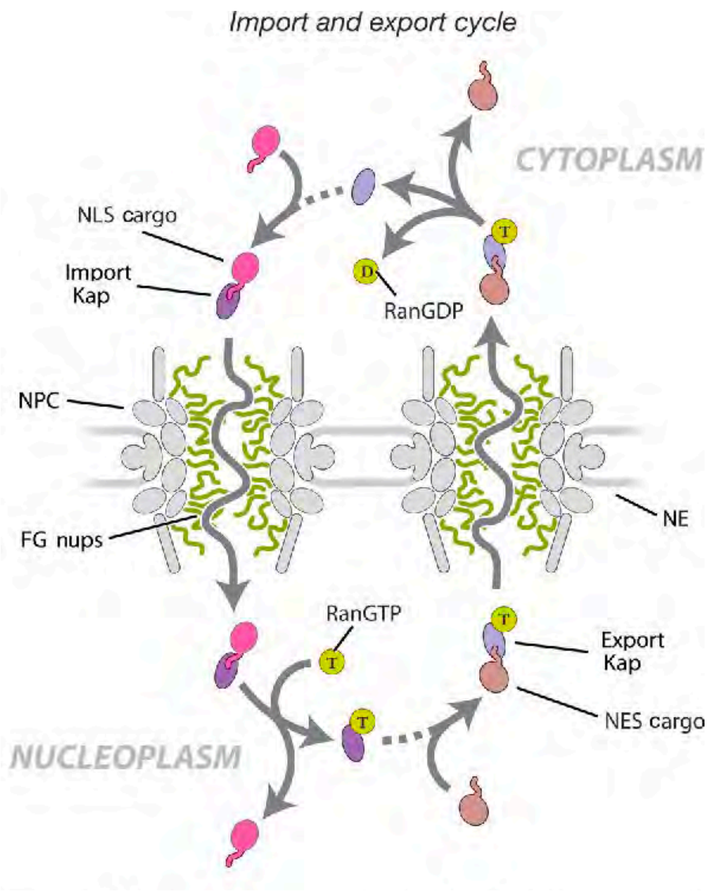
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

targeting domains



protein targeting
nuclear localization

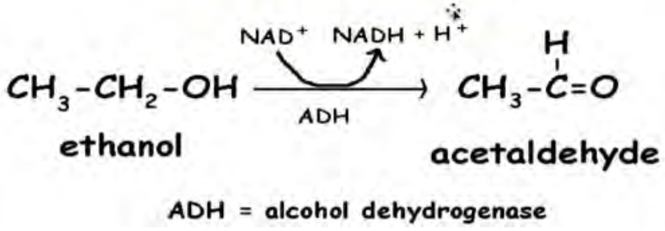
LECTURE 3
POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

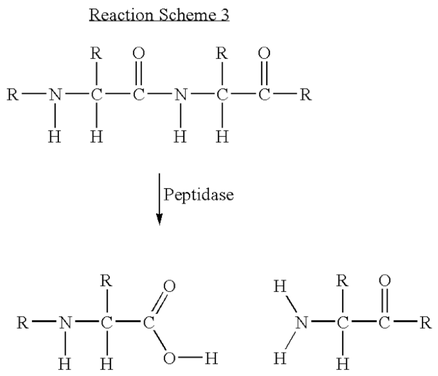
protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

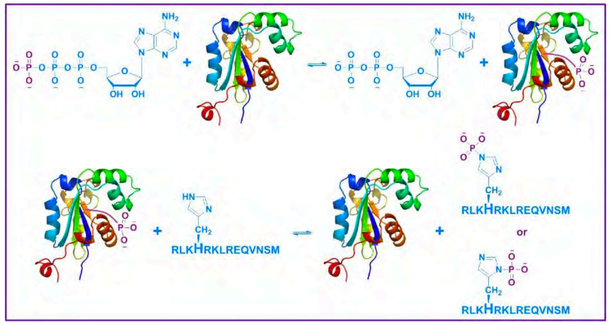
enzymatic domains



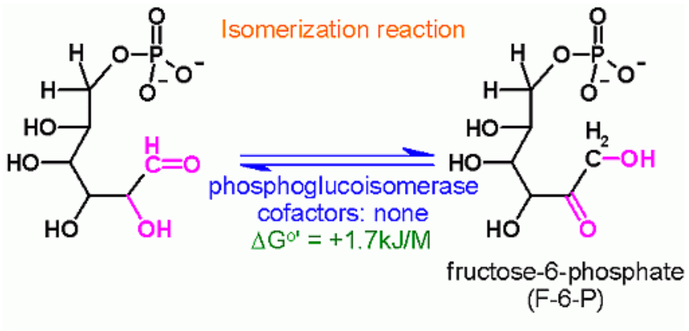
oxidoreductase
(oxidase/dehydrogenase)
changes reduction state



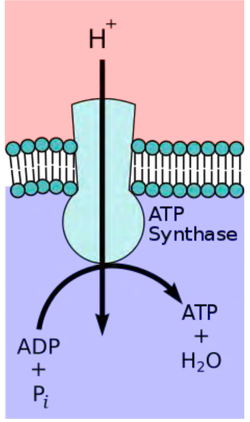
hydrolase
(endonuclease/protease)
breakdown using H2O



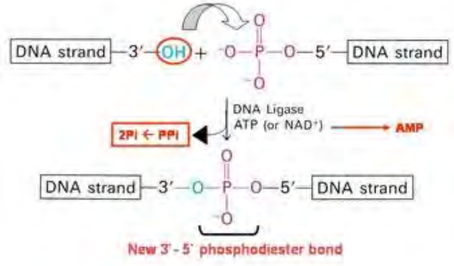
transferase
(kinase)
move a group



isomerase
(PGI)
same chemical formula



lyase
(synthase)
cleavage w/o H2O



ligase
(synthetase)
joins by condensation

LECTURE 3

POLYPEPTIDE **SYNTAX**

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence

LECTURE 3
POLYPEPTIDE **SYNTAX**

EXERCISE 2

create the following protein in benchling:

MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMS
VRLAEAMKRYGLNTNHRIVVCSENSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMNI
SQPTVVFVSKKGLQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYD
FVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILSV
VPFHHGFGMFTTLGYLICGFRVVLMYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTL
IDKYDLSNLHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPG
AVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLHS
GDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGEL
PAAVVVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILI
KAKKGGKSKL

use benchling to calculate the molecular mass and the isoelectric point of the sequence

will the protein be positively or negatively charged at neutral pH?

use http://www.compbio.dundee.ac.uk/jpred4/index.html to predict the protein secondary structure

use https://www.ebi.ac.uk/Tools/hmmer/search/hmmscan to predict the protein functional domains

use https://www.uniprot.org/ to BLAST the sequence and compare the domains identified

locate the PDB identifier number in uniprot and download the PDB file from https://www.rcsb.org/

predict the 3D structure using AlphaFold2 available in colab:
https://colab.research.google.com/github/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb

open both PDB files in Chimera and align the structures

select three residues where the structures are not in exact alignment and calculate the distances between the Calpha carbons

Amino acid structures
C1, Calpha carbons
hydrophobic - AGILPV
aromatic - FWY
neg charge - DE
pos charge - RHK
hydroxylic - ST
sulfur containing - CM
polar - NQ

protein structure
peptide bond
dihedral angles
phi (N-Ca)
psi (Ca-C1)
omega (C1-N) = 180deg unless proline (0deg)
protein folding
bond forces
stretching, bending, rotating
short range forces
Pauli repulsion, van der Waals' interactions
Electrostatic forces
Coulomb's law
interaction with solvent
Motif's
alpha helix
3.6 residues per turn
each residue 100deg, 1.5A
beta sheet
planar
isoelectric point
molecular weight

protein domains
binding domain - leucine zipper, TALEN
PTM domain
phosphorylation
methylation
ubiquitination
enzymatic domains
protease
kinase
targeting domains
NLS
signal peptide
anchoring sequence