

Donald Voet • Judith G. Voet • Charlotte W. Pratt

Fundamentals of Biochemistry

Second Edition

Chapter 5:

Proteins: Primary Structure

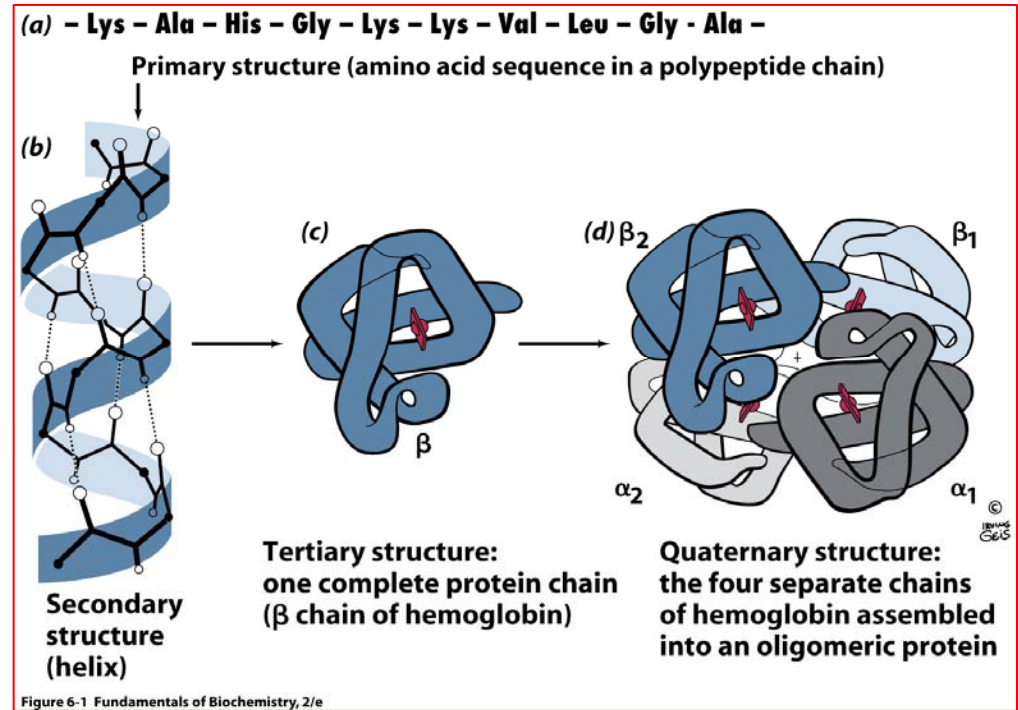
The great variation in structure and function among proteins



Protein structure

What is primary structure?

The amino acid sequence of its polypeptide chain



A chain

Gly-Ile-Val-Glu-Gln-Cys-Cys-Ala-Ser-Val-Cys-Ser-Leu-Tyr-Gln-Leu-Glu-Asn-Tyr-Cys-Asn
5 10 15 21

B chain

Phe-Val-Asn-Gln-His-Leu-Cys-Gly-Ser-His-Leu-Val-Glu-Ala-Leu-Tyr-Leu-Val-Cys-Gly-Glu-Arg-Gly-Phe-Phe-Tyr-Thr-Pro-Lys-Ala
5 10 15 20 25 30

Figure 5-1 Fundamentals of Biochemistry, 2/e
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Polypeptide diversity: theoretical possibilities are unlimited

Actual polypeptides are somewhat limited in size and composition

Size: at least 40 residues

The vast majority are between 100 and 1000 residues

Monomeric & multimeric (multisubunits)

Amino acid composition: average occurrence in proteins (Table 4-1)

Table 5-1 Compositions of Some Proteins

Protein	Amino Acid Residues	Subunits	Polypeptide Molecular Mass (<i>D</i>)
Proteinase inhibitor III (bitter gourd)	30	1	3,427
Cytochrome <i>c</i> (human)	104	1	11,617
Myoglobin (horse)	153	1	16,951
Interferon- γ (rabbit)	288	2	33,842
Chorismate mutase (<i>Bacillus subtilis</i>)	381	3	43,551
Triose phosphate isomerase (<i>E. coli</i>)	510	2	53,944
Hemoglobin (human)	574	4	61,986
RNA polymerase (bacteriophage T7)	883	1	98,885
Nucleoside diphosphate kinase (<i>Dictyostelium discoideum</i>)	930	6	100,764
Pyruvate decarboxylase (yeast)	2,252	4	245,456
Glutamine synthetase (<i>E. coli</i>)	5,616	12	621,264
Titin (human)	26,926	1	2,993,428

The largest known —→

Protein purification and analysis

Purification is a mandatory step for studying macromolecules
Starting from <0.1% to ~98% purity

A. General approach to purifying proteins

Genetic engineering: recombinant proteins

Protein source: organism, organs, cellular & subcellular locations

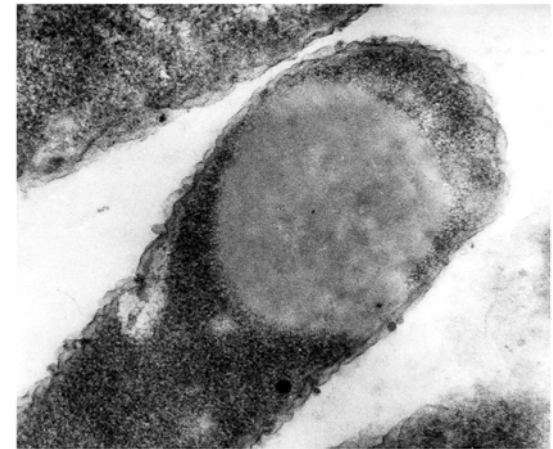


Figure 5-2 Fundamentals of Biochemistry, 2/e

Protein stabilization

- pH

- Temperature

- Degradative proteins

- Adsorption to surfaces: air-water interface, glass or plastic surfaces

- Long-term storage

http://www.biochem.arizona.edu/classes/bioc462/462a/NOTES/Protein_Properties/protein_purification.htm

http://www.bio.ic.ac.uk/research/nield/expertise/protein_purification.html

Protein assay

Assay: quantitative detection

Specific, sensitive & convenient

Enzymatic reaction: substrate & product

Physiological and artificial substrates

Coupled enzymatic reaction

Immunoassays: antibody

Radioimmunoassay (RIA)

Enzyme-linked immunosorbent assay (ELISA)

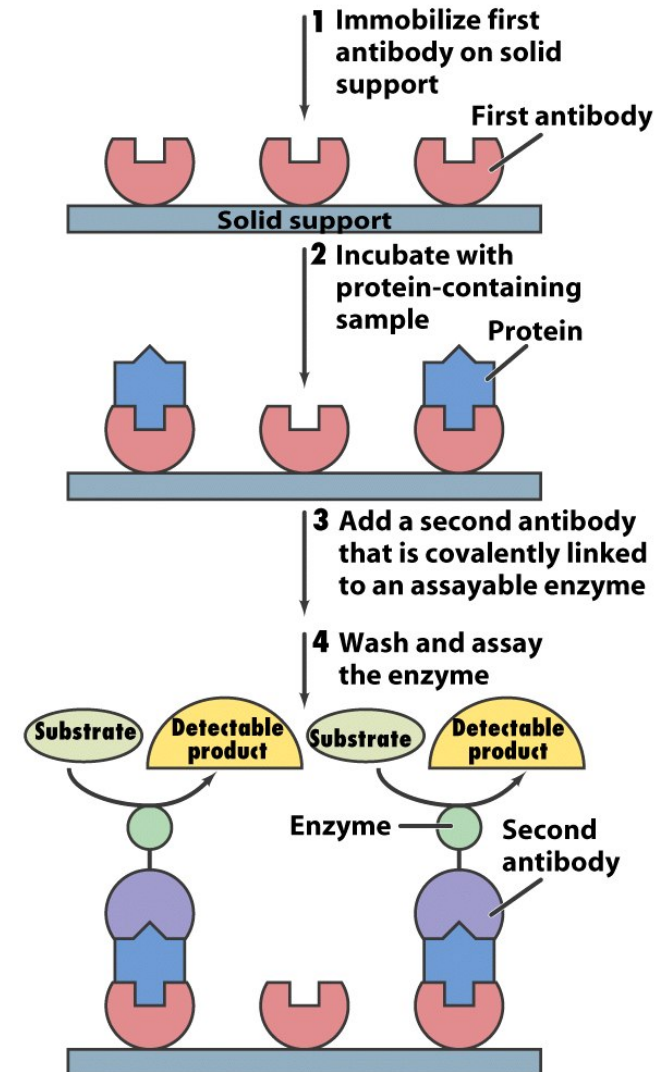


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Absorbance spectroscopy

Beer-Lambert law

$$A = \log(I_0/I) = \epsilon cl$$

A: absorbance (optical density)

I_0 : incident light intensity

I: transmitted intensity

ϵ : molar absorptivity (molar extinction coefficient)

c: molar concentration

l: the length of light path

Protein

UV assay: absorption at 280 nm (~1 mg/ml)

Chromophore: absorb light in the visible region

Dye-binding assay:

Bradford assay (Coomassie brilliant blue)L at 595 nm

UV-absorption spectra

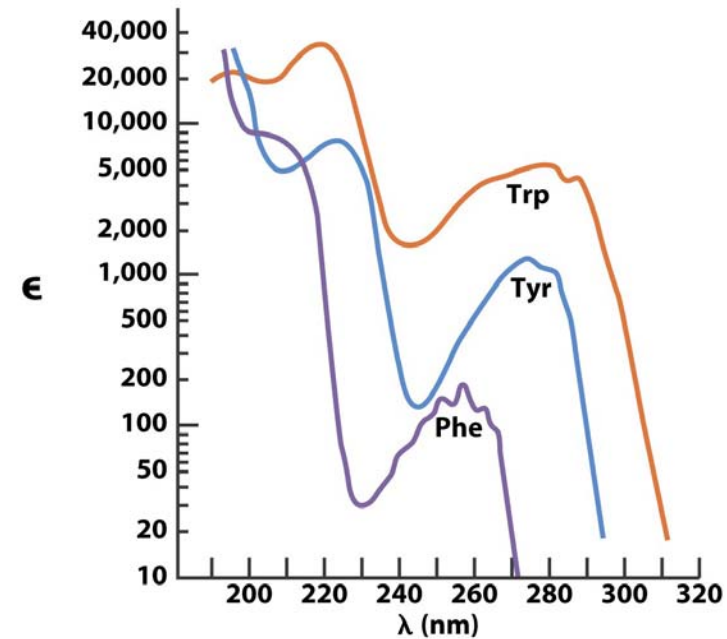
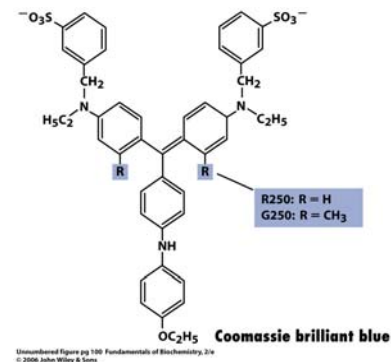
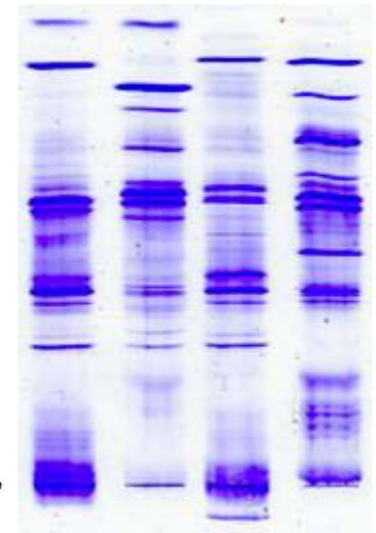


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Separation techniques

Purification of target protein by fractionation procedures

Selective elimination of the other components

Using physicochemical properties of proteins

<u>Protein characteristic</u>	<u>purification procedure</u>
Solubility	salting out
Ionic charge	ion exchange chromatography electrophoresis isoelectric focusing
Polarity	hydrophobic interaction chromatography
Size	gel filtration chromatography SDS-PAGE ultracentrifugation
Binding specificity	affinity chromatography

Salting in

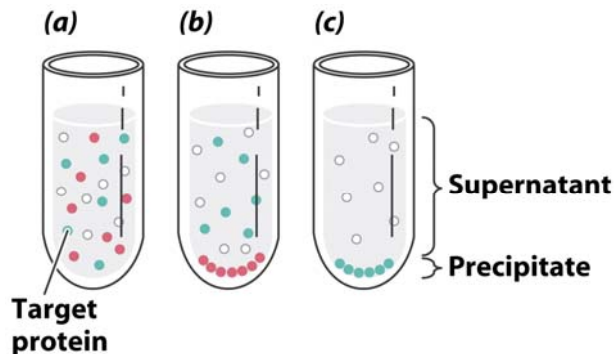
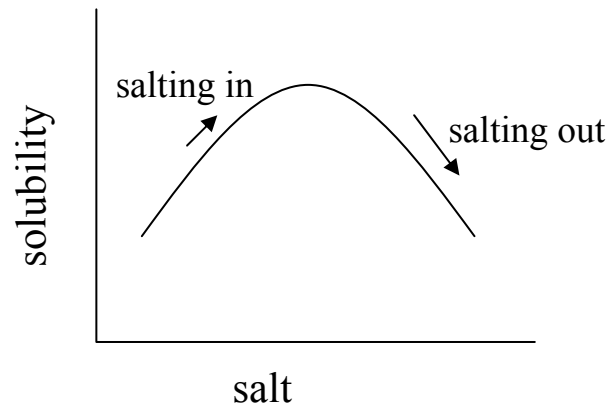


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Proteins are polyelectrolytes (polyionic polymers)
Proteins are least soluble when its net charge is zero

Table 5-2 Isoelectric Points of Several Common Proteins

Protein	pI
Pepsin	<1.0
Ovalbumin (hen)	4.6
Serum albumin (human)	4.9
Tropomyosin	5.1
Insulin (bovine)	5.4
Fibrinogen (human)	5.8
γ -Globulin (human)	6.6
Collagen	6.6
Myoglobin (horse)	7.0
Hemoglobin (human)	7.1
Ribonuclease A (bovine)	9.4
Cytochrome c (horse)	10.6
Histone (bovine)	10.8
Lysozyme (hen)	11.0
Salmine (salmon)	12.1

Table 5-2 Fundamentals of Biochemistry, 2/e
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Chromatography

Mobile phase: liquid

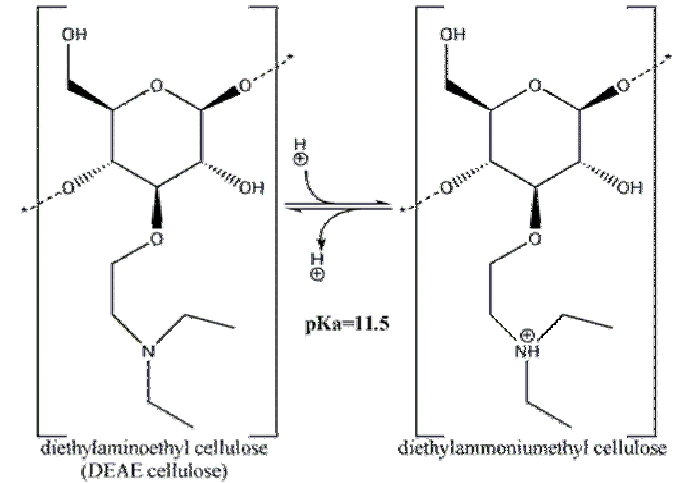
Stationary phase: porous solid matrix

From paper chromatography to HPLC

Ion-exchange chromatography

Anion exchanger: diethylaminoethyl (DEAE)

Cation exchanger: carboxy-methyl (CM) $-\text{CH}_2\text{-COO}^-$



HIC (hydrophobic interaction chromatography)

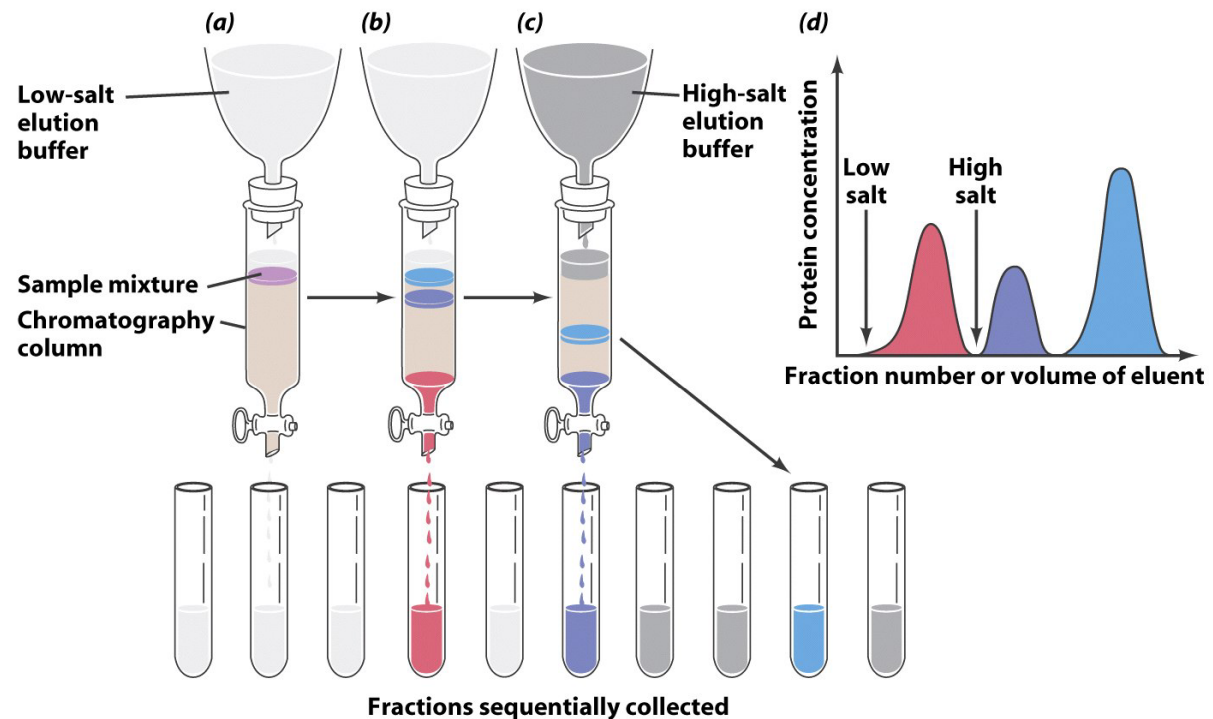


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Gel filtration chromatography

(size exclusion or molecular sieve chromatography)

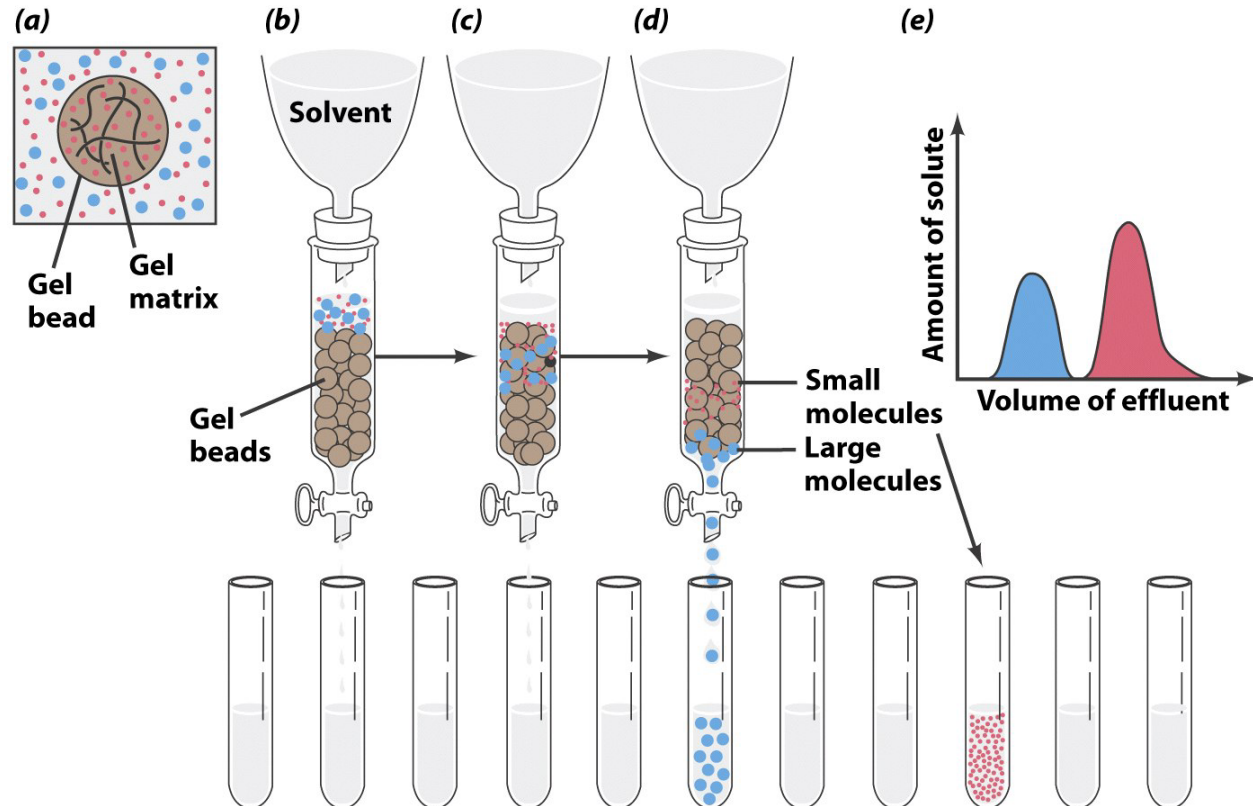
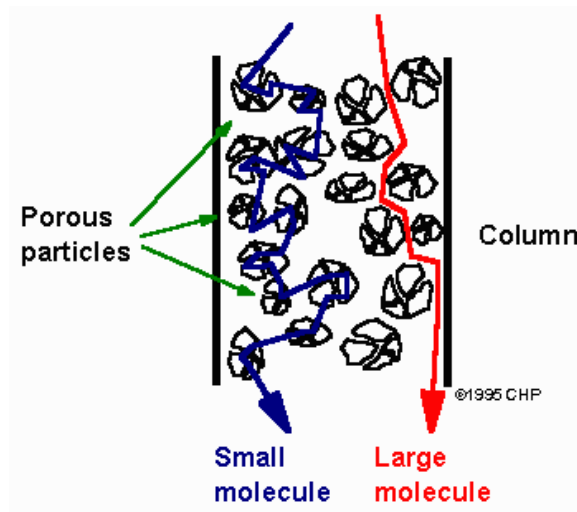


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Affinity chromatography

Ligand bound: cAMP, NADH, etc

Antibody bound: immunoaffinity chromatography

Metal bound: metal chelate affinity chromatography

Zn^{2+} , Ni^{2+}

his-tag column

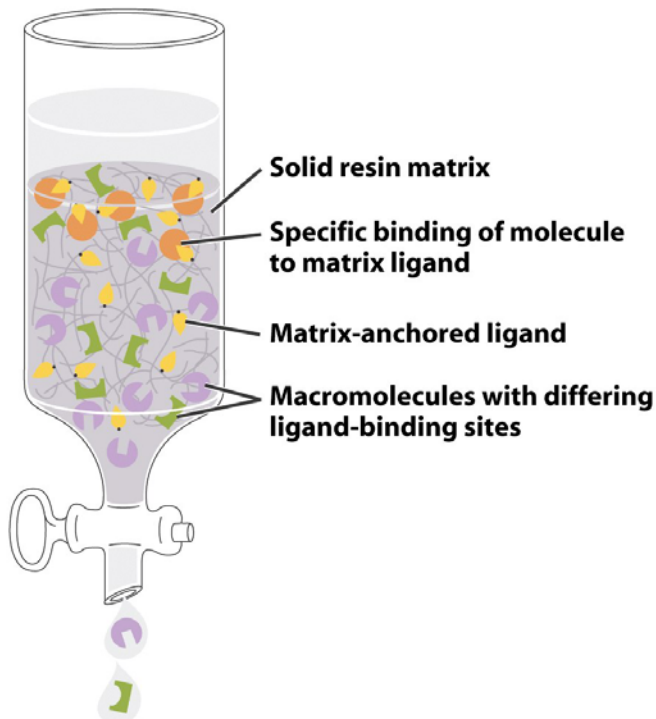
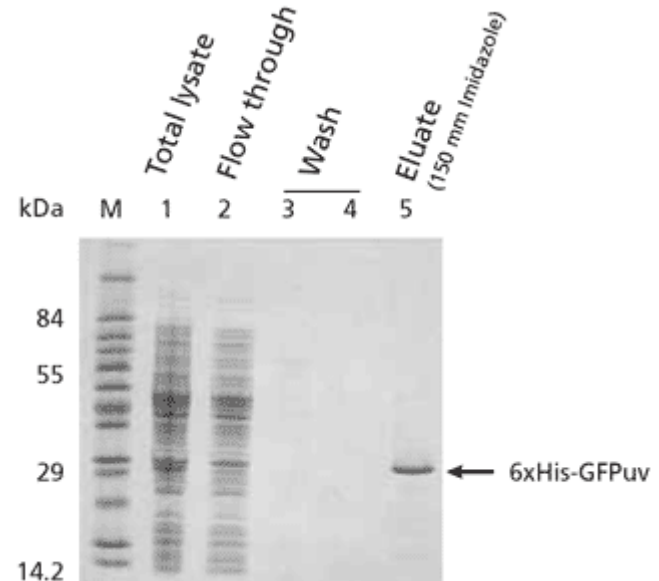


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Nickel Affinity Gel

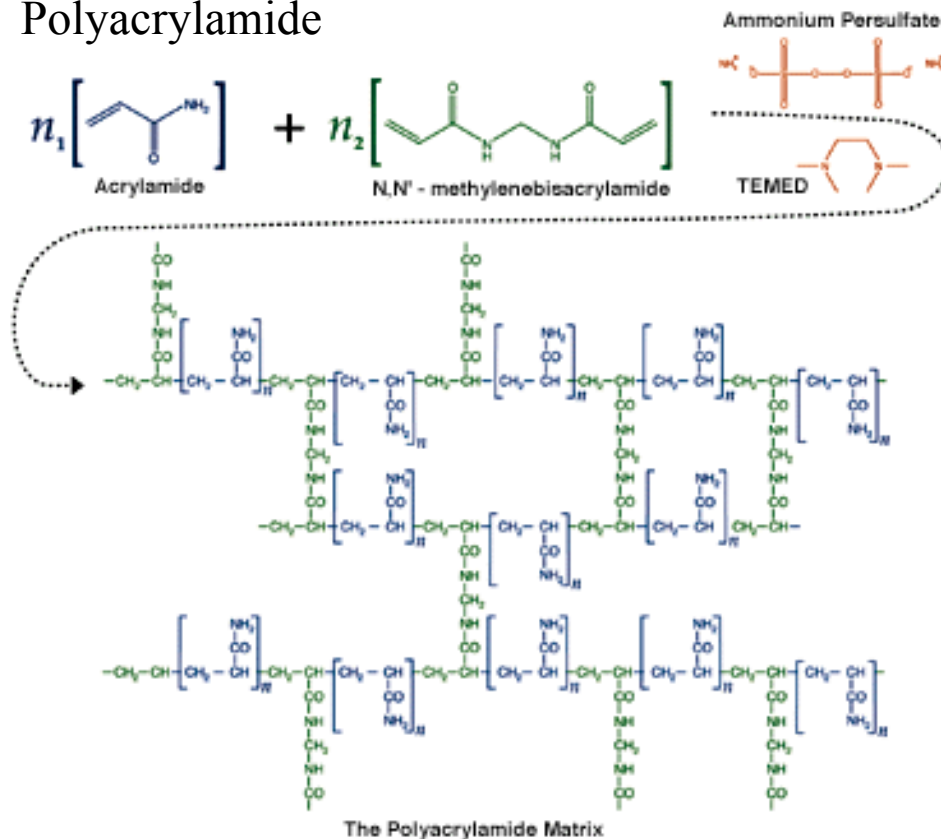


Electrophoresis

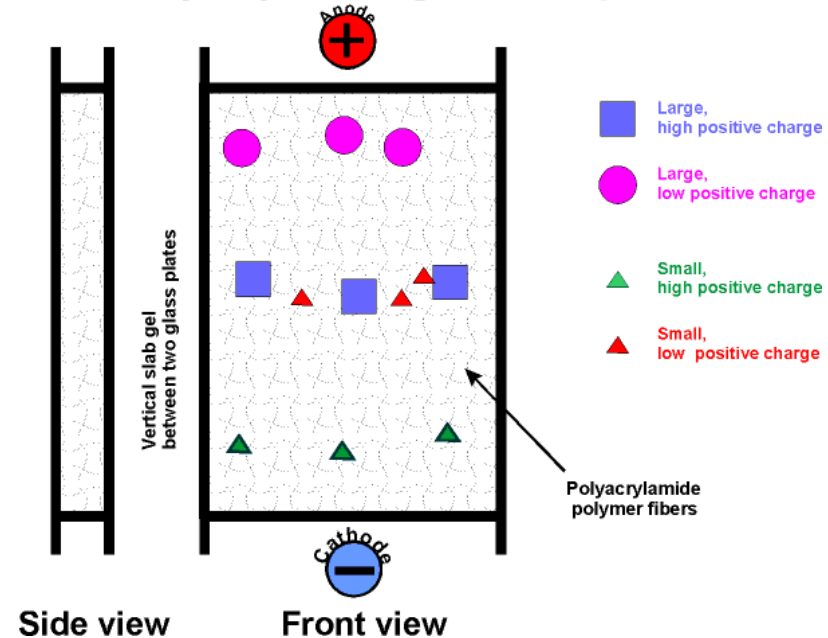
Polyacrylamide gel electrophoresis

Mobility difference depending on size, shape, electric charge

Polyacrylamide



Polyacrylamide gel electrophoresis



SDS-PAGE

SDS: sodium dodecylsulfate

Uniform binding of SDS to protein and denaturation

Net charge is equal in every protein

Separation depends on size

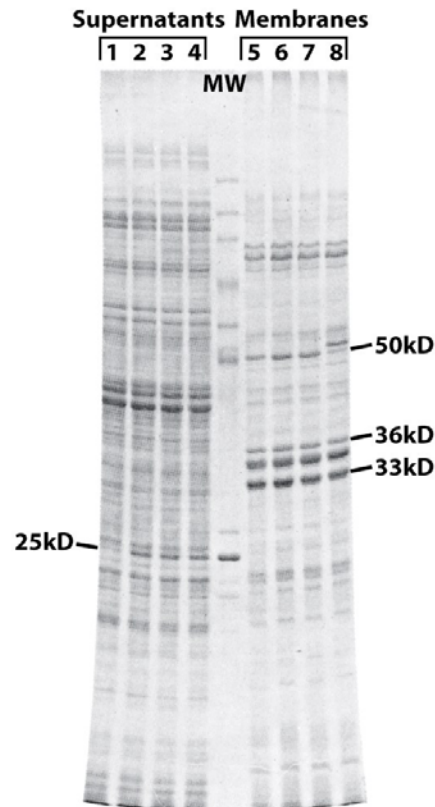
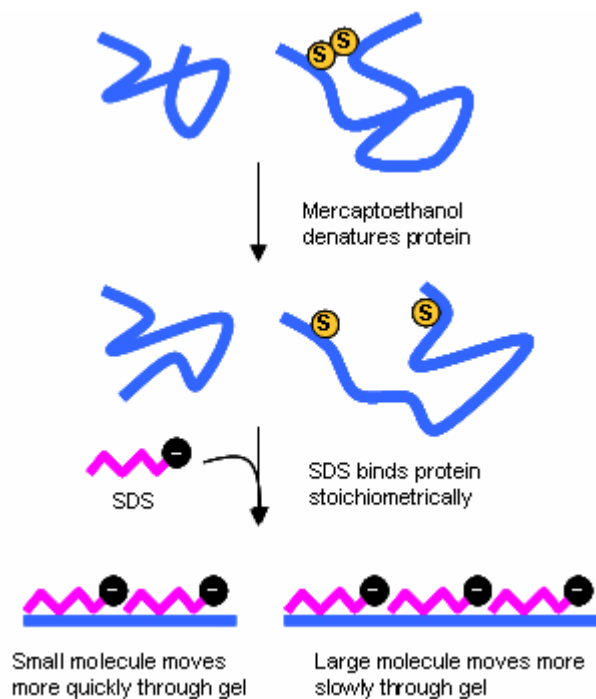


Figure 5-9 Fundamentals of Biochemistry, 2/e

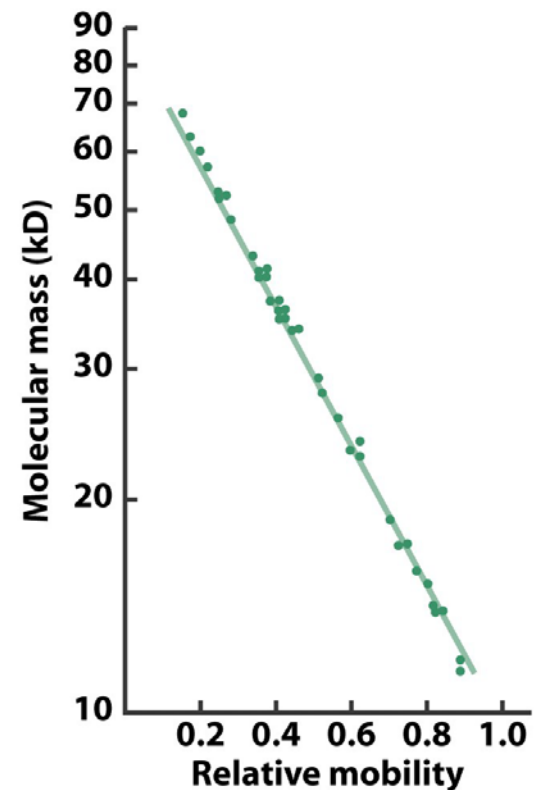


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Capillary electrophoresis

Electrophoresis in very thin capillary tubes (20-100 μm diameter)

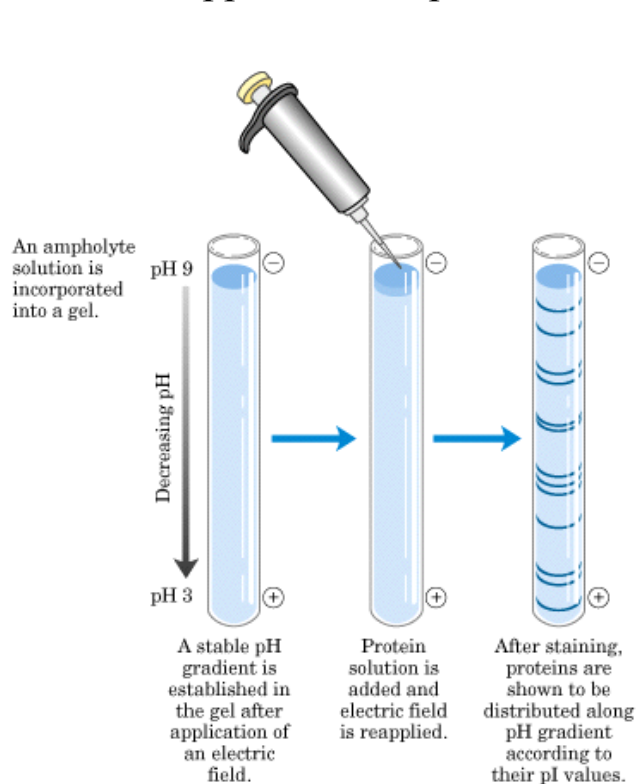
Dissipate heat and permit high electric fields

Fast separation

2D-PAGE

Isoelectric focusing (IEF) & SDS-PAGE

Application to proteomics



+ (pH 3)

- (pH 10)

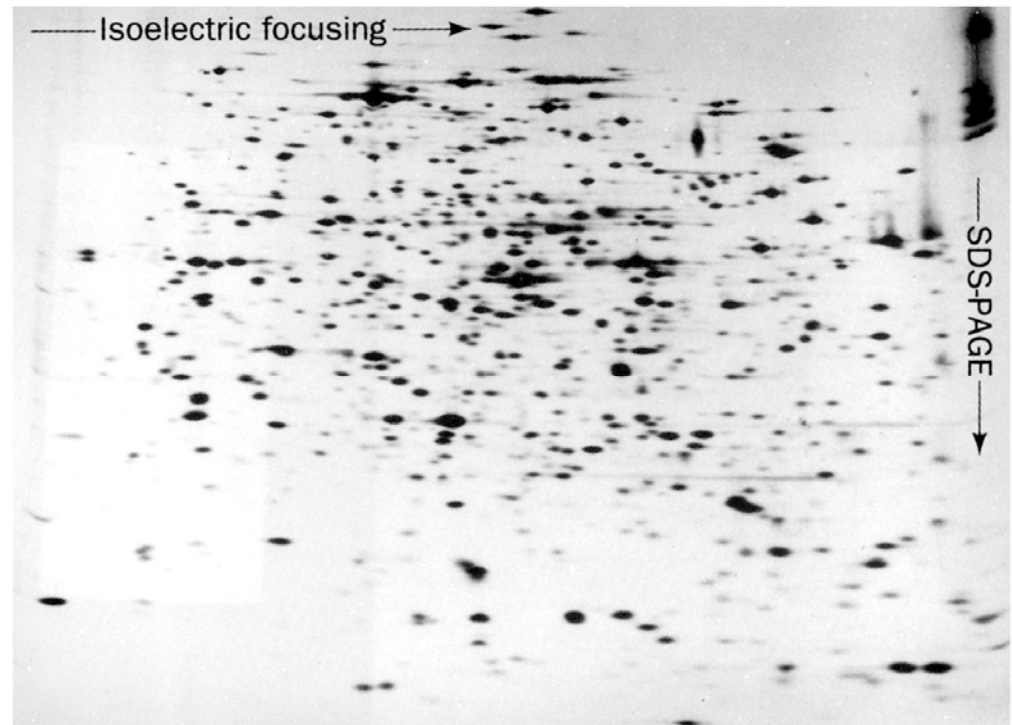
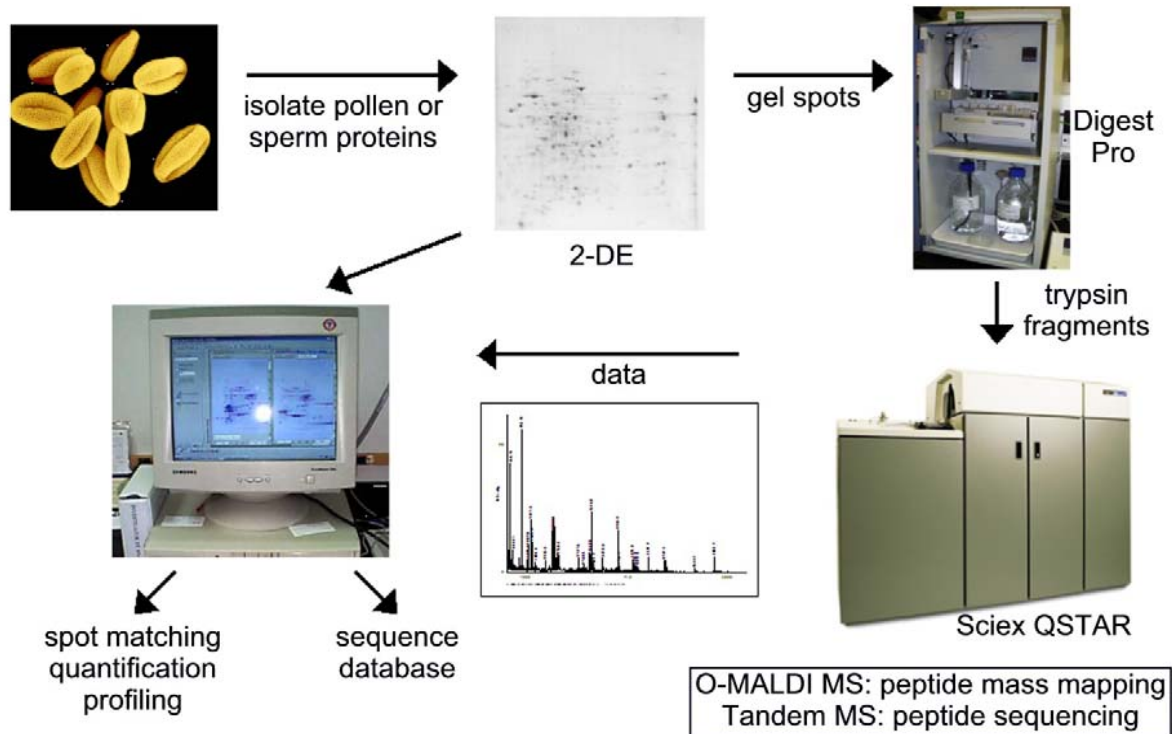


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Ultracentrifugation

Analytical

Preparative

Density gradient centrifugation (zonal centrifugation): sucrose, Percoll

Equilibrium density gradient centrifugation: CsCl

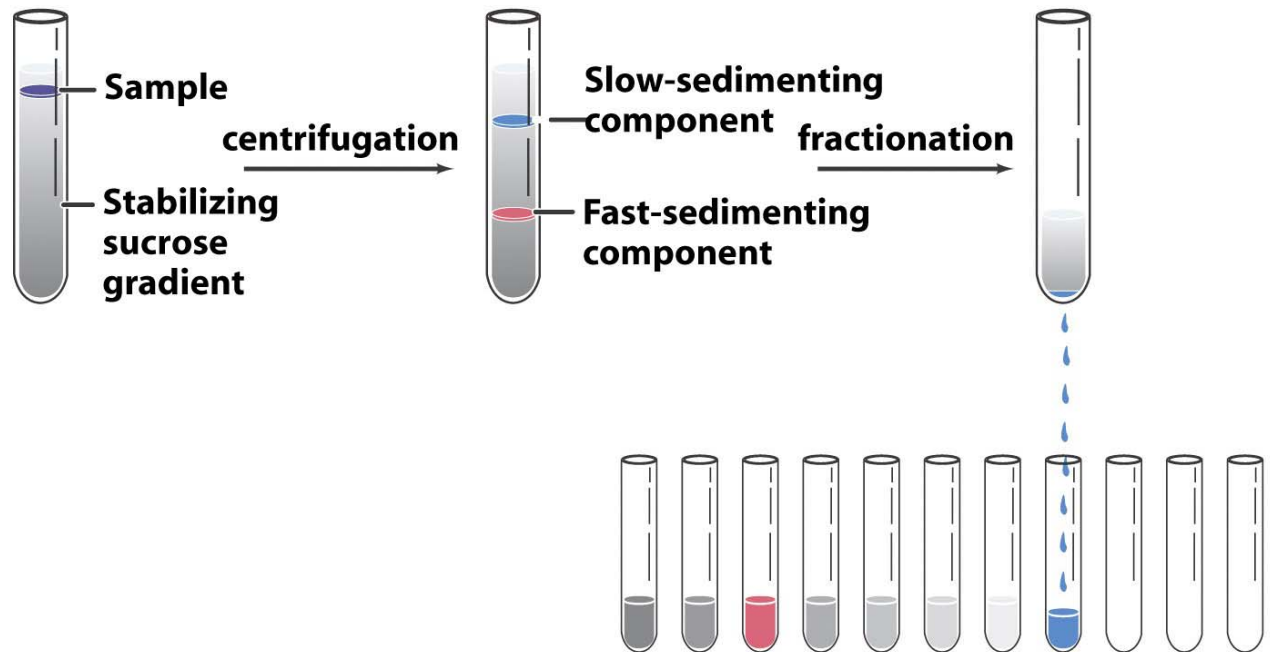
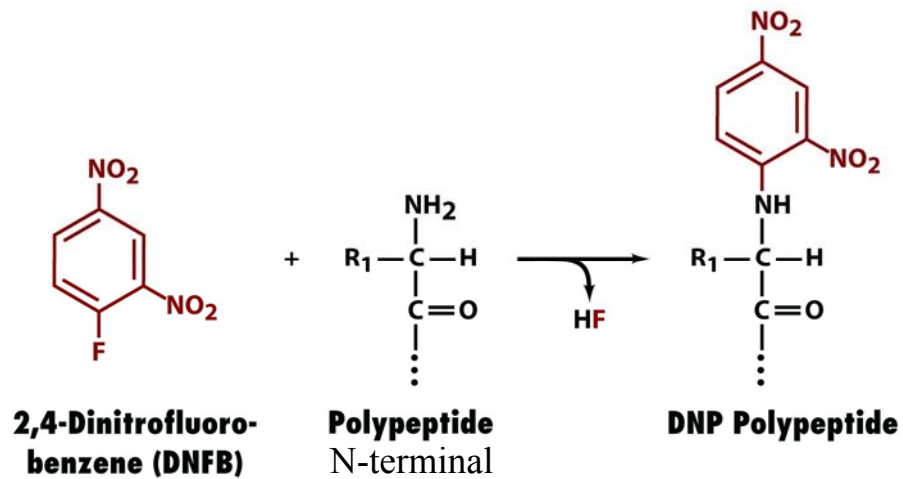
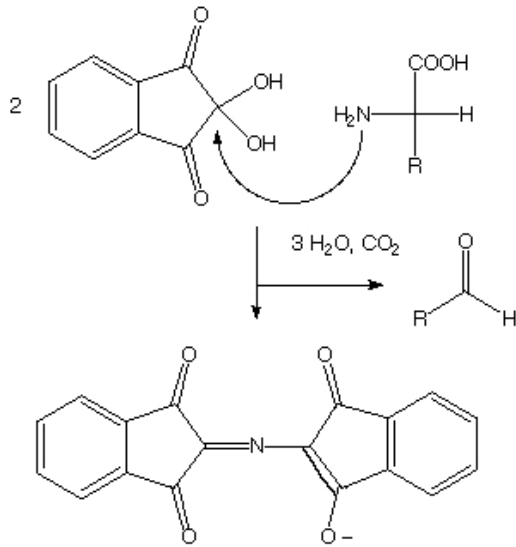


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Staining of amino acids and polypeptides



Protein sequencing

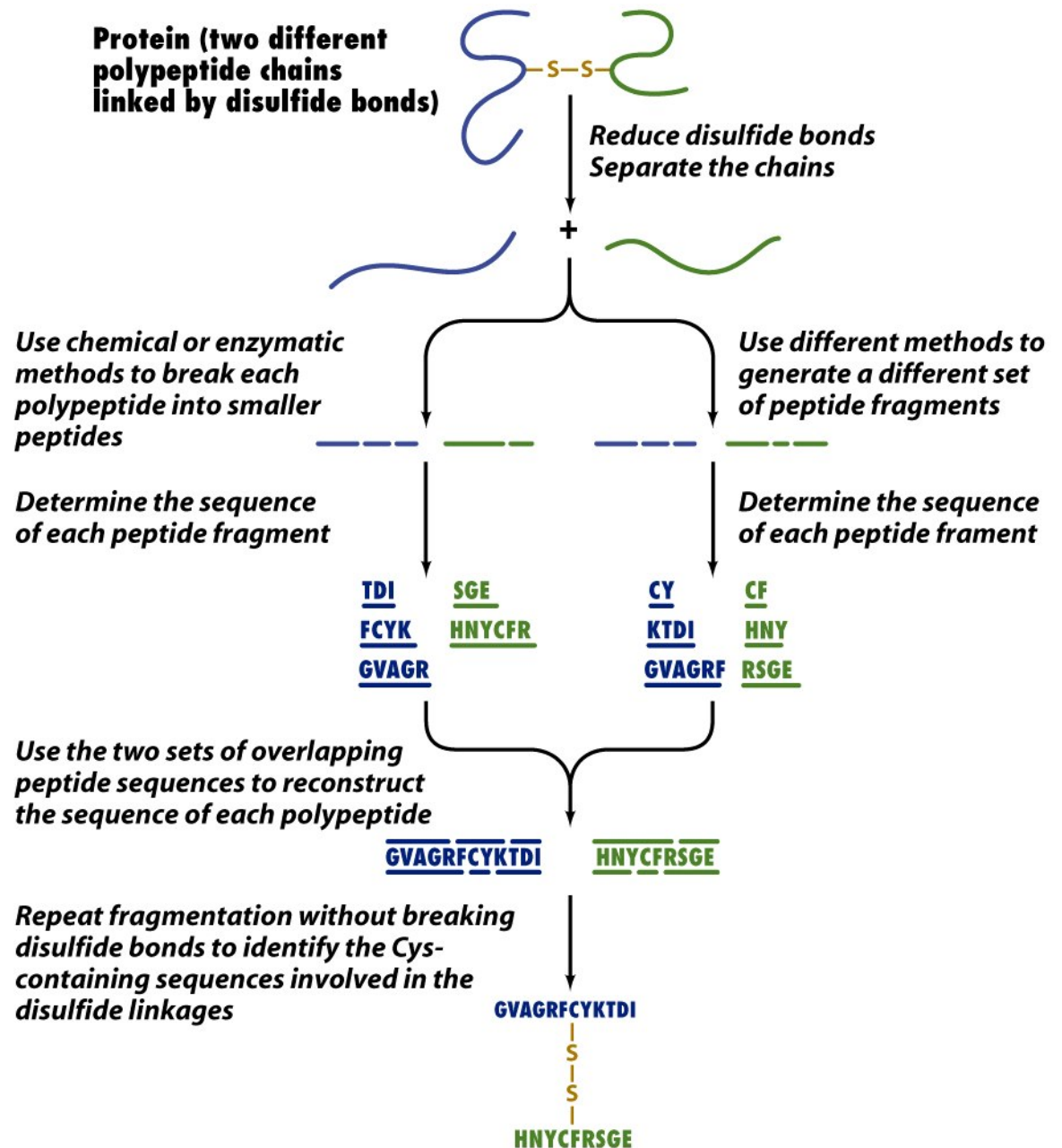


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Preliminary steps

N-terminal analysis: dansyl-chloride

differentiate subunits

Disulfide bond cleavage

Reduction with reducing reagent (2-mercaptoethanol or dithiothreitol): cystine to 2 cysteine

Alkylation with iodoacetate: Cys to S-carboxymethyl-Cys

Determination of amino acid composition: complete hydrolysis with HCl

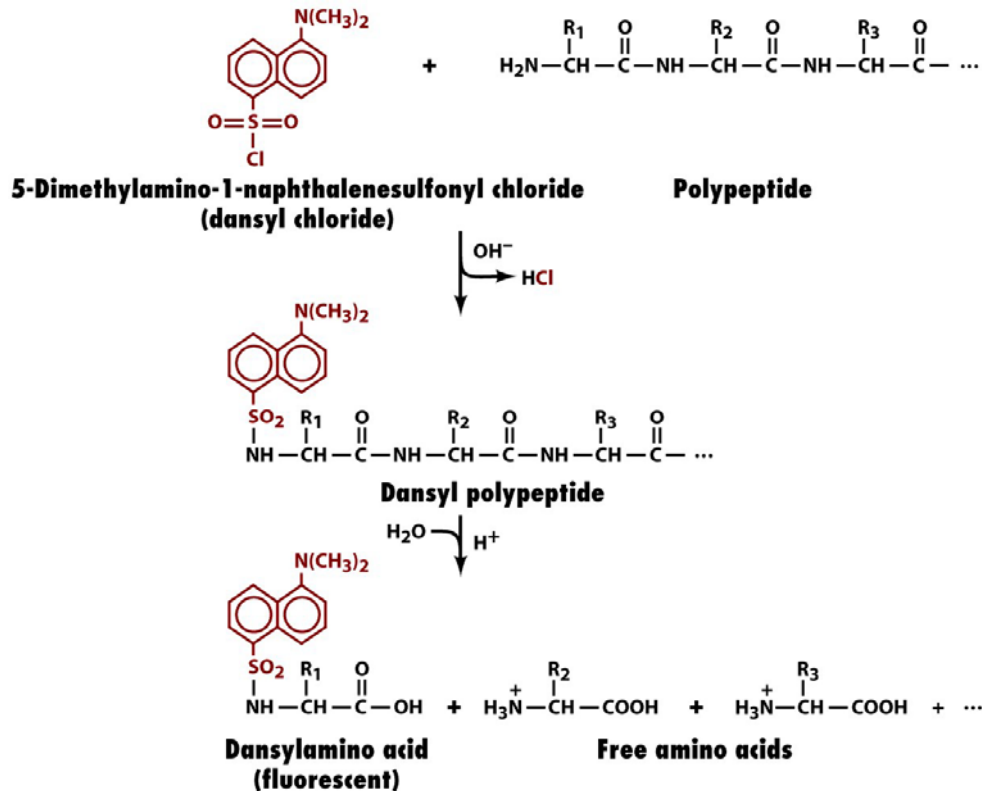


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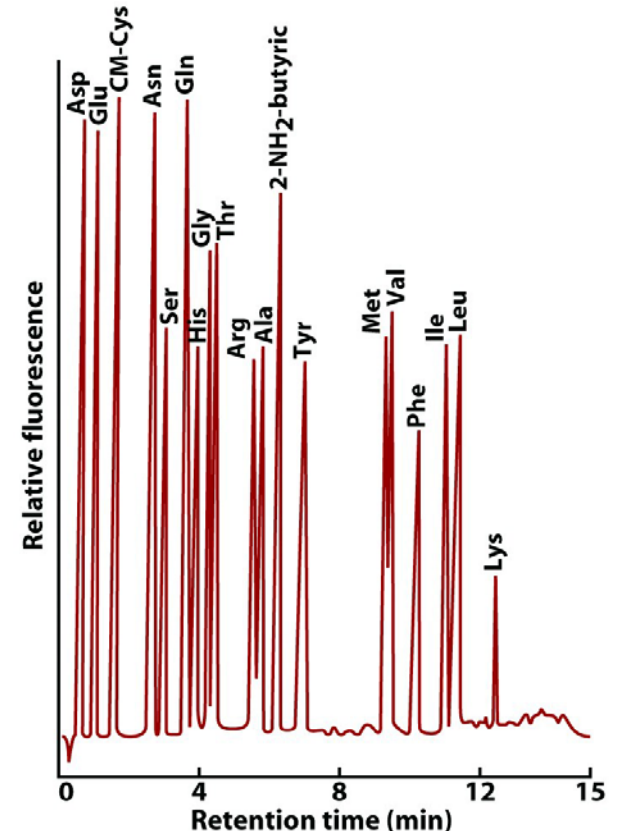
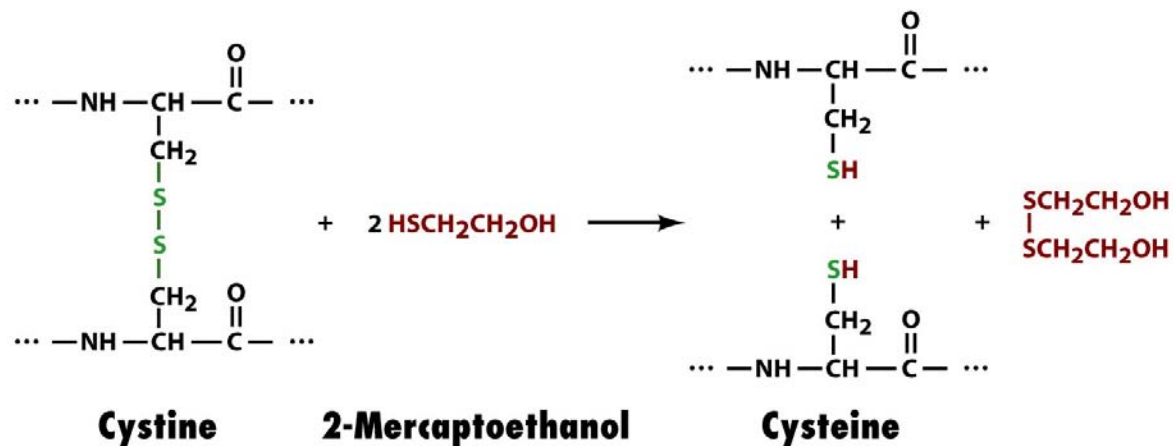
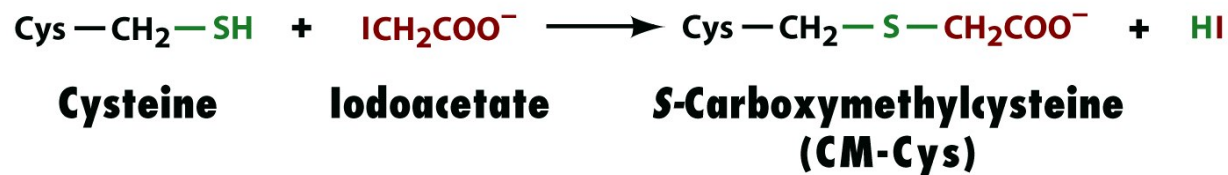


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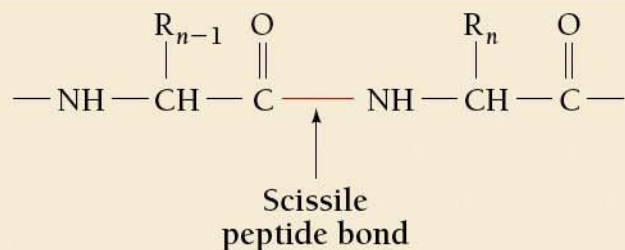
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Polypeptide cleavage

Endopeptidase

exopeptidase

Table 5-3 Specificities of Various Endopeptidases



Enzyme	Source	Specificity	Comments
Trypsin	Bovine pancreas	R_{n-1} = positively charged residues: Arg, Lys; $\text{R}_n \neq \text{Pro}$	Highly specific
Chymotrypsin	Bovine pancreas	R_{n-1} = bulky hydrophobic residues: Phe, Trp, Tyr; $\text{R}_n \neq \text{Pro}$	Cleaves more slowly for $\text{R}_{n-1} = \text{Asn, His, Met, Leu}$
Elastase	Bovine pancreas	R_{n-1} = small neutral residues: Ala, Gly, Ser, Val; $\text{R}_n \neq \text{Pro}$	
Thermolysin	<i>Bacillus thermoproteolyticus</i>	$\text{R}_n = \text{Ile, Met, Phe, Trp, Tyr, Val; } \text{R}_{n-1} \neq \text{Pro}$	Occasionally cleaves at $\text{R}_n = \text{Ala, Asp, His, Thr}$; heat stable
Pepsin	Bovine gastric mucosa	$\text{R}_n = \text{Leu, Phe, Trp, Tyr; } \text{R}_{n-1} \neq \text{Pro}$	Also others; quite nonspecific; pH optimum = 2
Endopeptidase V8	<i>Staphylococcus aureus</i>	$\text{R}_{n-1} = \text{Glu}$	

CNBr cleavage: C-side of Met residue

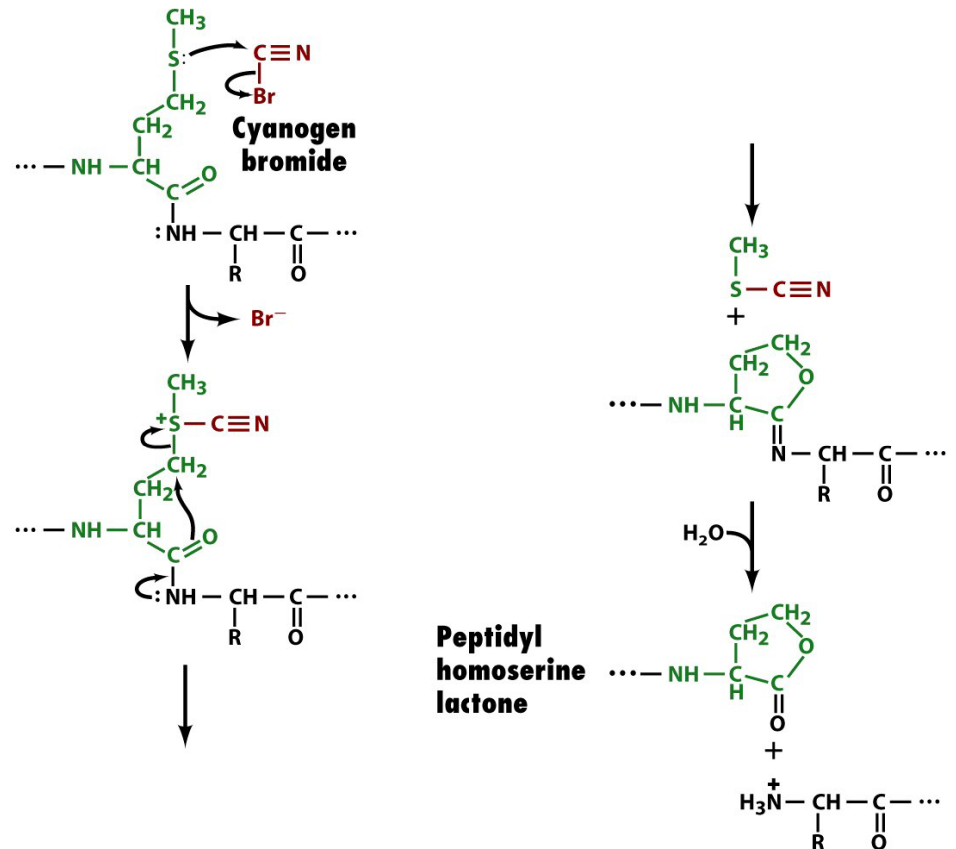


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Edman degradation

Sequential cleavage and identification of N-terminal residues

Solid-phase sequencing

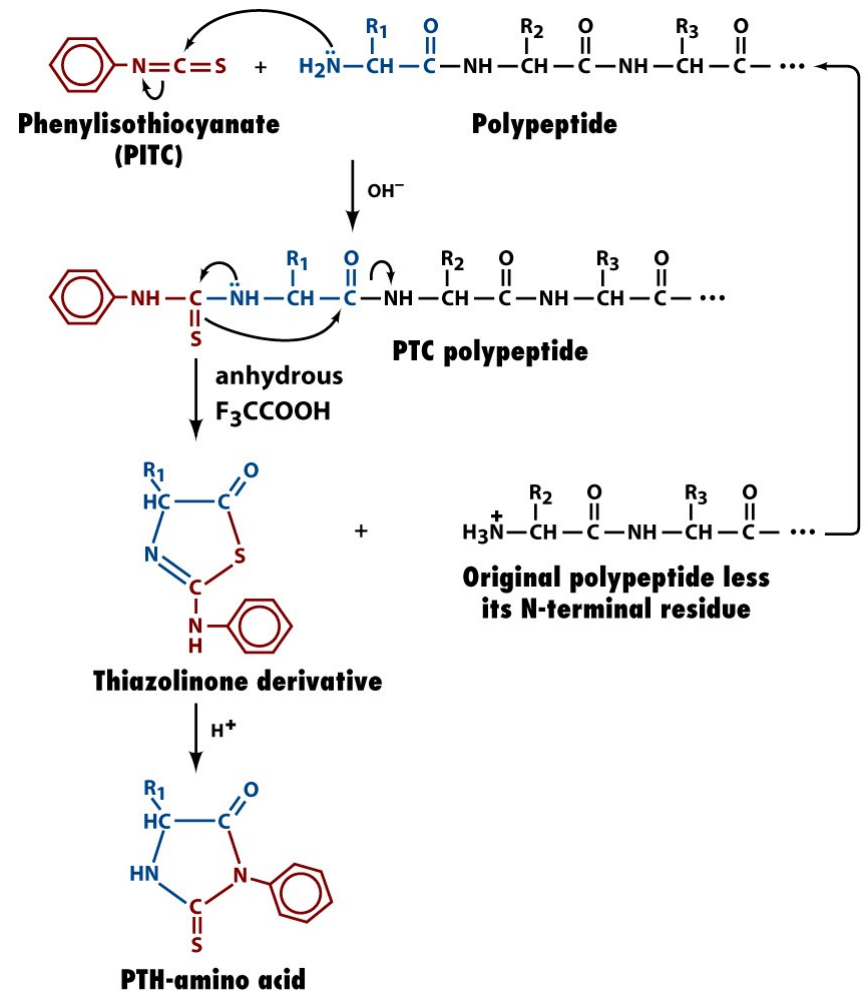


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Sequencing by mass spectrometry

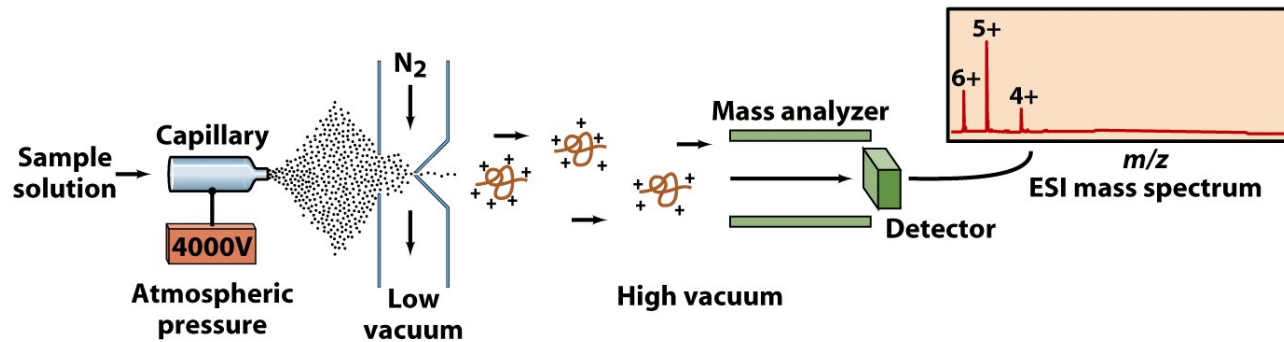


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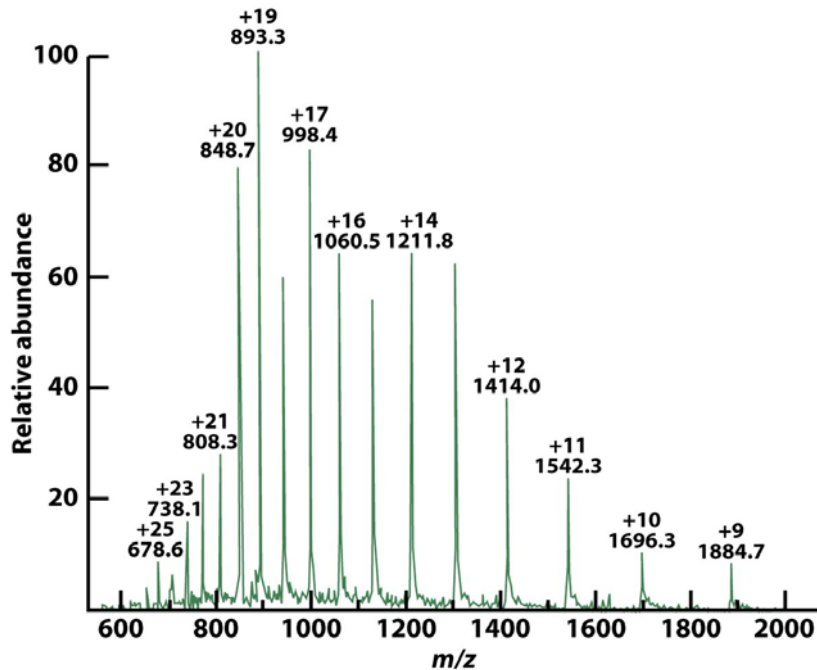


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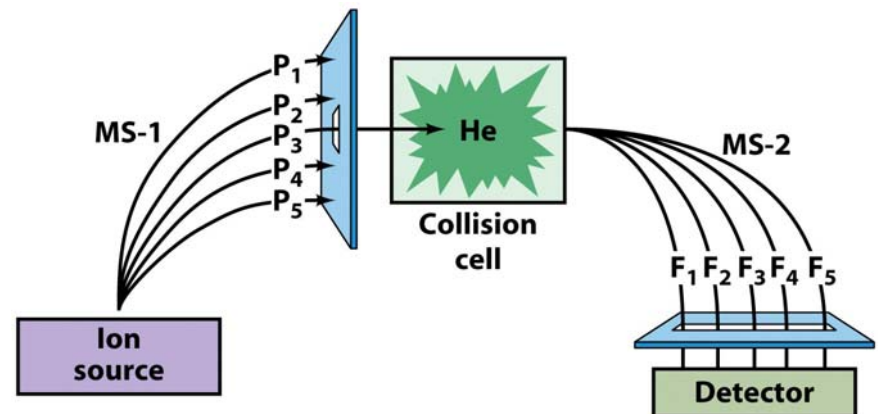


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Reconstructing the protein's sequence

Localization of disulfide bond

Cleave protein with its disulfide bonds intact

Alkylation and sequencing

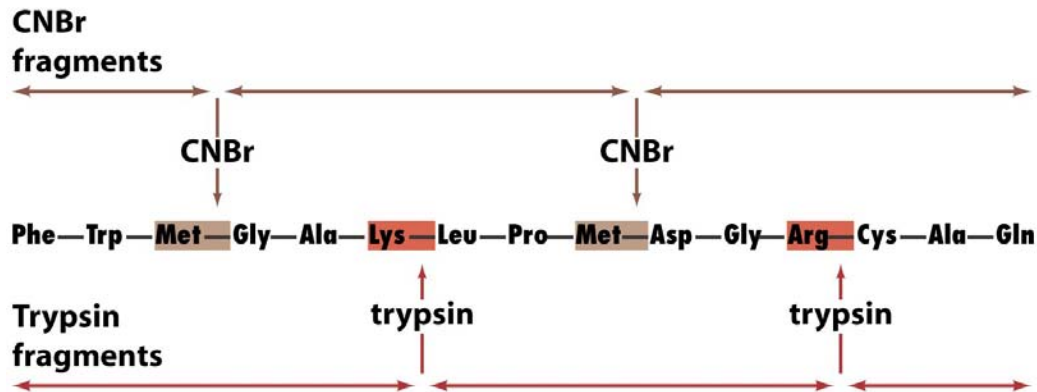


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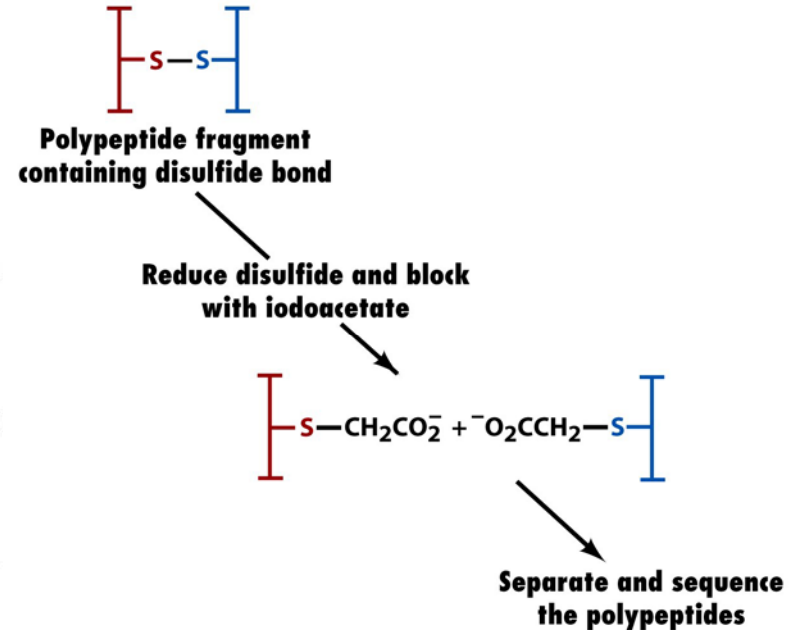


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Table 5-4 Internet Addresses for the Major Protein and DNA Sequence Data Banks

Data Banks Containing Protein Sequences

ExPASy Molecular Biology Server (Swiss-Prot): <http://au.expasy.org>

Protein Information Resource (PIR): <http://pir.georgetown.edu/>

Protein Research Foundation (PRF): <http://www4.prf.or.jp/>

UniProt: <http://www.ebi.uniprot.org/>

Data Banks Containing Gene Sequences

GenBank: <http://www.ncbi.nlm.nih.gov/Genbank/GenbankSearch.html>

European Bioinformatics Institute (EBI): <http://srs.ebi.ac.uk/>

DBGET/Integrated Database Retrieval System: <http://www.genome.ad.jp/dbget>

General information about the UniProt/Swiss-Prot entry		
Entry name	RSN_HUMAN	
Primary accession number	Q9HD89	
Entered in Swiss-Prot	Release 40, 16-OCT-2001	
Sequence was last modified	Release 40, 16-OCT-2001	
Annotations were last modified	Release 44, 05-JUL-2004	
Protein description		
Protein name	Resistin precursor	
Synonyms	Cysteine-rich secreted protein FIZZ3 Adipose tissue-specific secretory factor ADSF C/EBP-epsilon regulated myeloid-specific secreted cysteine-rich protein Cysteine-rich secreted protein A12-alpha-like 2 UNQ407/PRO1199	
Origin of the protein		
Gene	Gene name	RETN
	Synonyms	RSTN, FIZZ3, HXCP1
From	Homo sapiens (Human)[TaxID:9606]	
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

Figure 5-22 Fundamentals of Biochemistry, 2/e

Protein evolution

Darwinian evolution: many mutations are deleterious and disappear
some mutations are beneficial and survive

Protein sequence evolution

Sequence similarity

Multiple alignment

Evolution from a common ancestor

Evolutionary conservative: the meaning of biological importance

Sequence comparisons provide information on protein structure and function

Homologous proteins

Invariant residues: essential

Conservatively substituted: similar side chains

Hypervariable: nonspecific

If cyt.c is important, why not identical?

the random nature of mutational processes: neutral drift

depends on tolerable or intolerable

		-9	-5	-1	1	5	10	15	20	25	30	35	40	45																																			
Mammals	Human, chimpanzee					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	S	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Rhesus monkey					α	G	D	V	E	K	G	K	K	I	F	I	M	K	C	S	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Horse					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Donkey					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Cow, pig, sheep					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Dog					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Rabbit					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	California gray whale					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
Great gray kangaroo					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	I	N	G	I	F	G	R	K	T	G	Q	A	
Other vertebrates	Chicken, turkey					α	G	D	I	E	K	G	K	K	I	F	V	Q	K	C	S	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Pigeon					α	G	D	I	E	K	G	K	K	I	F	V	Q	K	C	S	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Pekin duck					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	S	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Snapping turtle					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	N	G	L	I	G	R	K	T	G	Q	A
	Rattlesnake					α	G	D	V	E	K	G	K	K	I	F	T	M	K	C	S	Q	C	H	T	V	E	K	G	G	K	H	K	T	G	P	N	L	H	G	L	F	G	R	K	T	G	Q	A
	Bullfrog					α	G	D	V	E	K	G	K	K	I	F	V	Q	K	C	A	Q	C	H	T	C	E	K	G	G	K	H	K	V	G	P	N	L	Y	G	L	I	G	R	K	T	G	Q	A
	Tuna					α	G	D	V	A	K	G	K	K	T	F	V	Q																															

Source: After Dickerson, R.E., *Sci. Am.* 226(4): 58-72 (1972), with corrections from Dickerson, R.E., and Timkovich, R., in Boyer, P.D. (Ed.), *The Enzymes* (3rd ed.), Vol. 11, pp. 421-422, Academic Press (1975). Table copyrighted © by Irving Geis.

45	50	55	60	65	70	75	80	85	90	95	100	104																																																
P	G	G	S	Y	T	A	A	N	K	N	K	G	I	I	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	V	G	I	K	K	K	E	E	R	A	D	L	I	A	Y	L	K	K	A	T	N	E
P	G	G	S	Y	T	A	A	N	K	N	K	G	I	I	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	V	G	I	K	K	K	E	E	R	A	D	L	I	A	Y	L	K	K	A	A	N	E
P	G	G	T	Y	T	D	A	N	K	N	K	G	I	T	W	K	E	E	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	T	E	R	E	D	L	I	A	Y	L	K	K	A	T	N	E
P	G	G	S	Y	T	D	A	N	K	N	K	G	I	T	W	K	E	E	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	T	E	R	E	D	L	I	A	Y	L	K	K	A	T	N	E
P	G	G	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	E	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	G	E	R	E	D	L	I	A	Y	L	K	K	A	T	N	E
P	G	G	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	E	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	T	G	E	R	A	D	L	I	A	Y	L	K	K	A	T	K	E
V	G	F	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	D	E	R	A	D	L	I	A	Y	L	K	K	A	T	N	E
V	G	F	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	E	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	G	E	R	A	D	L	I	A	Y	L	K	K	A	T	N	E
P	G	G	T	Y	T	D	A	N	K	N	K	G	I	I	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	G	E	R	A	D	L	I	A	Y	L	K	K	A	T	N	E
E	G	F	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	S	E	R	V	D	L	I	A	Y	L	K	D	A	T	S	K
E	G	F	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	A	E	R	A	D	L	I	A	Y	L	K	Q	A	T	A	K
E	G	F	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	S	E	R	A	D	L	I	A	Y	L	K	D	A	T	A	K
E	G	F	S	Y	T	E	A	N	K	N	K	G	I	T	W	G	E	E	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	A	E	R	A	D	L	I	A	Y	L	K	D	A	T	S	K
V	G	F	S	Y	T	A	A	N	K	N	K	G	I	I	W	G	D	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	V	F	T	G	L	S	K	K	K	E	R	T	N	L	I	A	Y	L	K	E	K	T	A	A
A	G	F	S	Y	T	D	A	N	K	N	K	G	I	T	W	G	E	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	G	E	R	Q	D	L	I	A	Y	L	K	S	A	C	S	K
E	G	Y	S	Y	T	D	A	N	K	S	K	G	I	V	W	N	N	D	T	L	M	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	I	K	K	K	G	E	R	Q	D	L	V	A	Y	L	K	S	A	T	S	-
Q	G	F	S	Y	T	D	A	N	K	S	K	G	I	T	W	Q	Q	E	T	L	R	I	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	L	K	K	K	S	E	R	Q	D	L	I	A	Y	L	K	K	T	A	A	S
P	G	F	S	Y	S	N	A	N	K	A	K	G	I	T	W	G	D	D	T	L	F	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	V	F	A	G	L	K	K	A	N	E	R	A	D	L	I	A	Y	L	K	E	S	T	K	-
P	G	F	S	Y	S	N	A	N	K	A	K	G	I	T	W	Q	D	D	T	L	F	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	V	F	A	G	L	K	K	A	N	E	R	A	D	L	I	A	Y	L	K	Q	A	T	K	-
A	G	F	A	Y	T	N	A	N	K	A	K	G	I	T	W	Q	D	D	T	L	F	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	L	K	K	P	N	E	R	G	D	L	I	A	Y	L	K	S	A	T	K	-
A	G	F	A	Y	T	N	A	N	K	A	K	G	I	T	W	Q	D	D	T	L	F	E	Y	L	E	N	P	K	K	Y	I	P	G	T	K	M	I	F	A	G	L	K	K	P	N	E	R	G	D	L	I	A	Y	L	K	S	A	T	K	-
Q	G	Y	S	Y	T	D	A	N	I	K	N	V	L	W	D	E	N	N	M	S	E	Y	L	T	N	P	X	K	Y	I	P	G	T	K	M	A	F	G	G	L	K	K	E	K	D	R	N	D	L	I	T	Y	L	K	K	A	C	E	-	
Q	G	Y	S	Y	T	D	A	N	K	R	A	G	V	E	W	A	E	P	T	M	S	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	A	F	G	G	L	K	K	A	K	D	R	N	D	L	V	T	Y	M	L	E	A	S	K	
D	G	Y	A	Y	T	D	A	N	K	Q	K	G	I	T	W	D	E	N	T	L	F	E	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	A	F	G	G	L	K	K	D	K	D	R	N	D	I	I	T	F	M	K	E	A	T	A	-
A	G	Y	S	Y	S	A	A	N	K	N	K	A	V	E	W	E	E	N	T	L	Y	D	Y	L	L	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	K	A	T	S	S
A	G	Y	S	Y	S	A	A	N	K	N	K	A	V	T	W	G	E	D	T	L	Y	E	Y	L	L	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	E	R	A	D	L	I	A	Y	L	K	D	S	T	E	-
A	G	Y	S	Y	S	A	A	N	K	N	M	A	V	I	W	E	E	N	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	E	R	A	D	L	I	A	Y	L	K	T	S	T	A	-
A	G	Y	S	Y	S	T	A	N	K	N	M	A	V	I	W	E	E	K	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	E	S	T	A	-
A	G	Y	S	Y	S	A	A	N	K	N	K	A	V	E	W	E	E	K	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	E	A	T	A	-
P	G	Y	S	Y	S	A	A	N	K	N	R	A	V	I	W	E	E	K	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	E	A	T	A	-
P	G	Y	S	Y	S	A	A	N	K	N	M	A	V	I	W	G	E	N	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	E	R	A	D	L	I	A	Y	L	K	E	A	T	A	-
A	G	Y	S	Y	S	A	A	N	K	N	M	A	V	Q	W	G	E	N	T	L	Y	A	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	E	A	T	A	-
A	G	Y	S	Y	S	A	A	N	K	N	M	A	V	Q	W	G	E	N	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	E	S	T	A	-
P	G	Y	S	Y	S	A	A	N	K	N	M	A	V	N	W	G	E	N	T	L	Y	D	Y	L	E	N	P	X	K	Y	I	P	G	T	K	M	V	F	P	G	L	X	K	P	Q	D	R	A	D	L	I	A	Y	L	K	E	S	T	A	-
6	1	2	3	1	2	5	1	1	2	6	4	3	2	7	1	4	5	2	2	5	4	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	5	1	2	2	1	6	9	2	1	7	2	2	2	2	2	2	2	6	4	5	4

6 1 2 3 1 2 5 1 1 2 6 4 3 2 7 1 7 4 5 2 2 5 4 1 1 3 1 1 1 1 1 1 1 1 1 1 3 1 5 1 2 2 1 6 9 2 1 7 2 2 2 2 2 2 2 6 4 4 5 4

Hydrophilic, acidic: **D** Asp **E** Glu

Hydrophilic, basic: **H** His **K** Lys **R** Arg **X** TrimethylLys

Polar, uncharged: **B** Asn or Asp **G** Gly **N** Asn **Q** Gln
S Ser **T** Thr **W** Trp **Y** Tyr **Z** Gln or Glu

Hydrophobic: **A** Ala **C** Cys **F** Phe **I** Ile **L** Leu
M Met **P** Pro **V** Val

Table 5-5 part 2 Fundamentals of Biochemistry, 2/e

Constructing phylogenetic trees

Evolutionary relationship

Computer program to construct phylogeny

Quantitative measure of the degree of relatedness

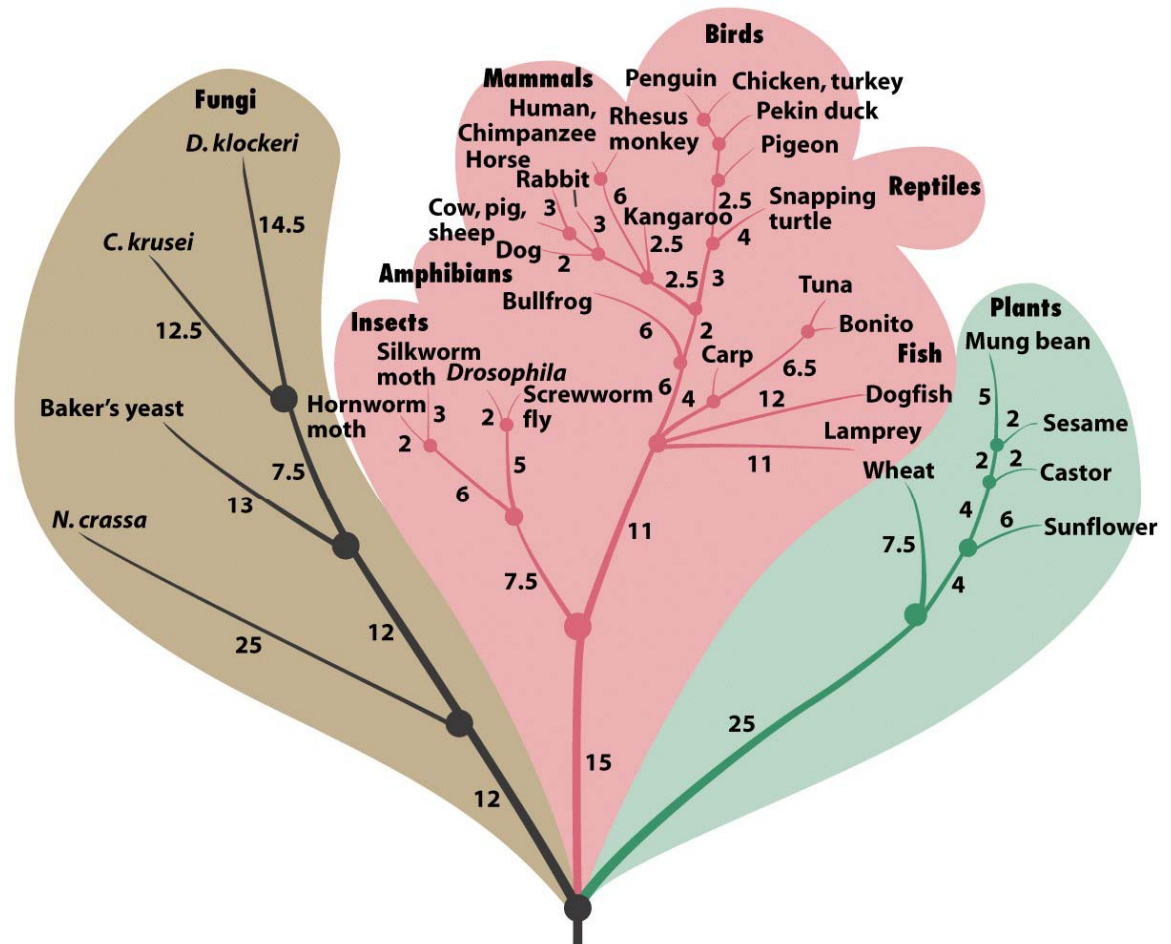


Figure 5-23 Fundamentals of Biochemistry, 2/e
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Protein evolve at characteristic rates

Protein sequence difference plotted against the time when the species diverged

The linear nature of mutation rate depending on proteins

Mutations accumulate at a constant rate over a geological time scale

Protein sequences do not reveal the complete story of evolution

The proteins of human and chimpanzee are >99% identical

Why then so different between them?

Differences in regulation and expression (time and space)

Rearrangements and duplications of genes, giving rise to new proteins

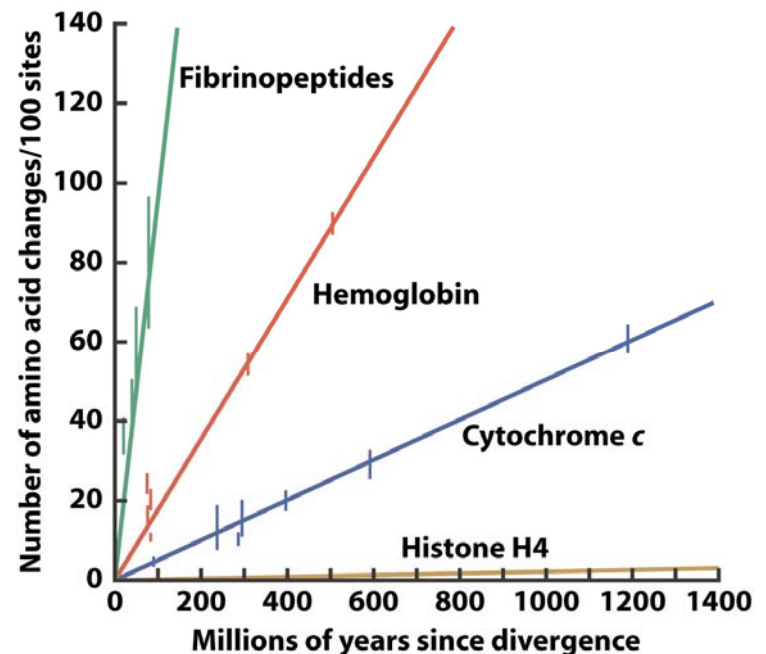


Figure 5-24 Fundamentals of Biochemistry, 2/e
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Gene duplication and protein families

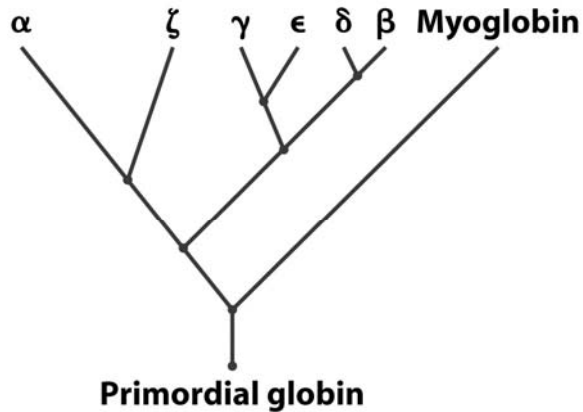
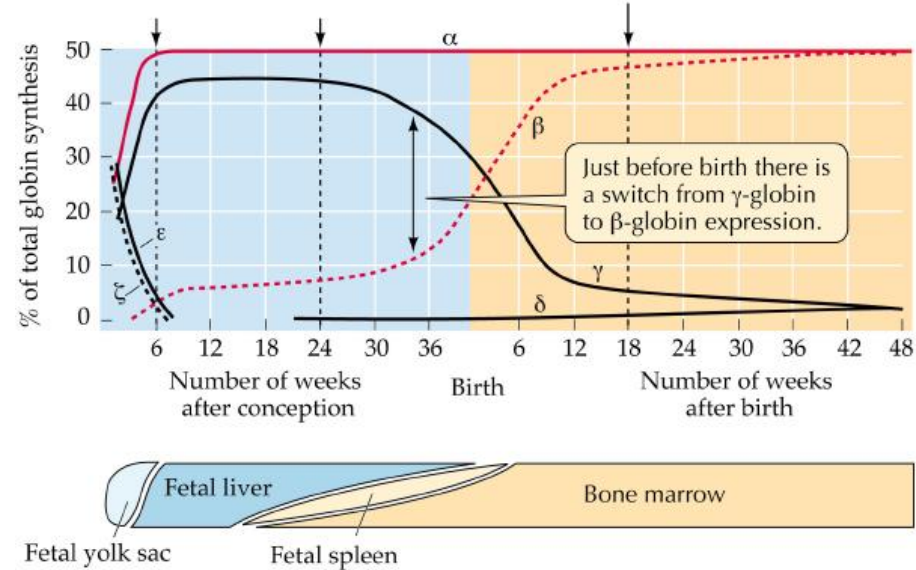


Figure 5-25 Fundamentals of Biochemistry, 2/e
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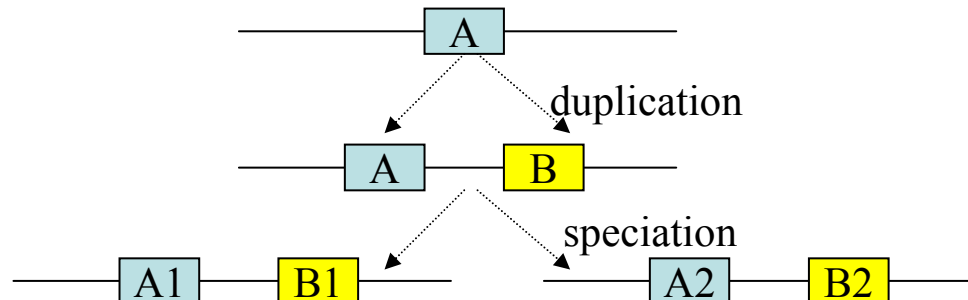
Homologous genes: derived from a common ancestor

orthologs: separated by speciation, similar functions and structure

paralogs: separated by a duplication event, different but related functions

xenologs: lateral transfer between two organisms

***pseudogenes



Protein modules

Modules of ~40-100 amino acid residues
exon shuffling

(a) Fibronectin



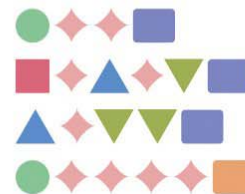
(b) Blood clotting proteins

Factors VII, IX, X, and protein C

Factor XII

Tissue-type plasminogen activator

Protein S



Key

- ▲ Fibronectin domain 1
- Fibronectin domain 2
- Fibronectin domain 3
- γ-Carboxyglutamate domain
- ◆ Epidermal growth factor domain
- Serine protease domain
- ▼ Kringle domain
- Unique domain