

Outline

- Universal features of life among bacteria, archaea, eukaryotes
- Gap between data and knowledge
- How is research conducted? Learning to think independently.
- Cell biology integrates several approaches to understand how cells live, respond to stimuli and divide.

Approaches and methods:

Cell biology: microscopy to visualize where and when a process occurs

Biochemistry: purify to demonstrate activity of (a) molecule(s)

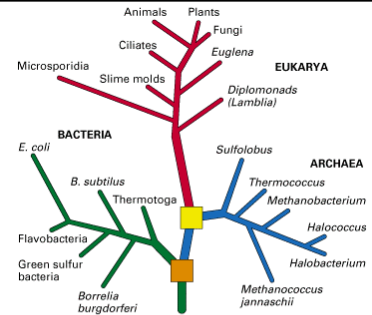
Genetic: study function in organism using mutants

Genetics & biochemistry: study mechanism of molecule activity

Bioinformatics: Use data of genes, proteins, microarrays, proteomics (protein interactions) to get inferences or clues to function

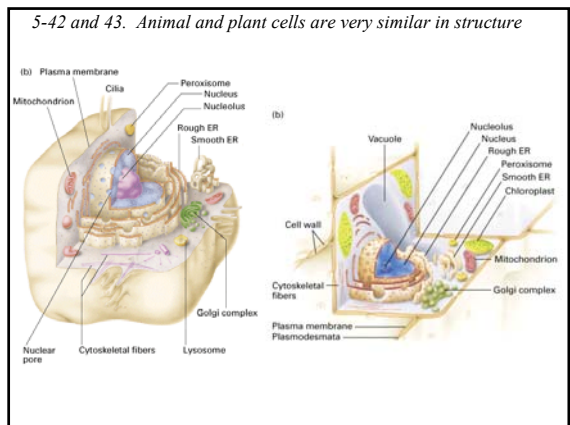
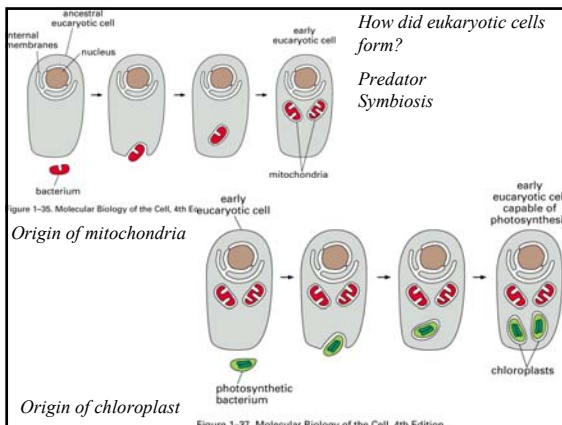
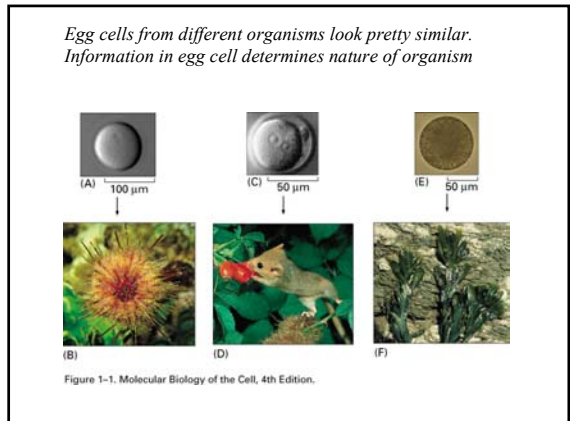
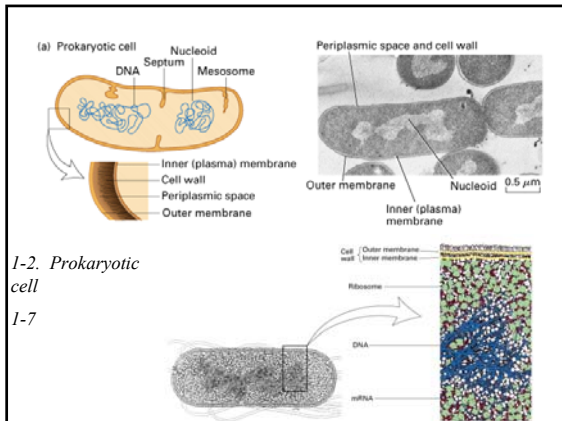
Universal features of life and of cells

1-5. 3 kingdoms of organisms are related through common sequences of their r-RNAs

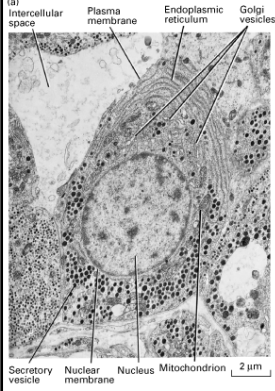


1-21. Alberts

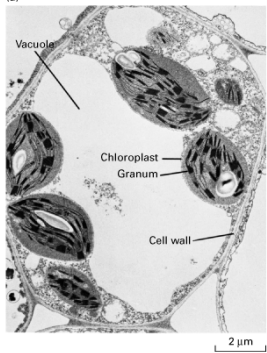
- Presumed common progenitor of all extant organisms
- Presumed common progenitor of archaea, bacteria, and eukaryotes



5-42. Animal cell: rat pituitary



5-43. Plant leaf cell (differentiated)



Brunet et al 2003. TiCB

Gap between data and knowledge. Proteomics is a powerful tool though other studies are needed to reveal how the dynamic structures interact with one another and remodel in response to stimuli.



The task of managing, analyzing and visualizing such volumes of data requires the skills of the bioinformaticist, but even more critical is the participation of the cell biologist who must form and evaluate hypotheses based on these data. In this context, two key aspects of bioinformatics in MS-based proteomics can be highlighted. First, how bioinformatics enables the generation of proteomic data by overcoming technical hurdles. Second, how bioinformatics can enable the cell biologist to interpret proteomic data.

Analysis of the cell organelles in various conditions will be needed to understand the dynamic nature of integrated cell functions.

Discovery begins with a question

1. Observation by Microscopy

What is that structure?

What does it do?

How?

2. We have a complete set of genes and predicted proteins for yeast, fly, plant, or human.

What is the function of each gene?

Then one generates a working hypothesis
or
collect useful information to form a hypothesis

A model or idea of how a process might work.

Test hypothesis.

One chooses an approach & gives a rationale

• *Approach is a way or means to reach a destination.*

*e.g. genetic
biochemical*

Approach is not = method.

• *Rationale : reason, a logical basis*

Genetics: study of mutants [why?]

Forward genetics

Reverse genetics

Biochemistry: [why?]

Choose a material /organism

Give rationale for choice

And plan the method

e.g. Plan a genetic approach.

a biochemical approach- study of the function of a molecule.

extract & purify

study the chemical activity of the molecule

Cell biological approach

Get results and analyze them. Interpret results

What do results tell you? Interpret independently.

Be a detective, look for clues

Ask if results are convincing.

To interpret results confidently,
one needs to know the technique
and its limitations

Review of methods used in cell biology

Microscopy, in Alberts ch 9

Biochemical methods

Genetic

Molecular

Bioinformatics

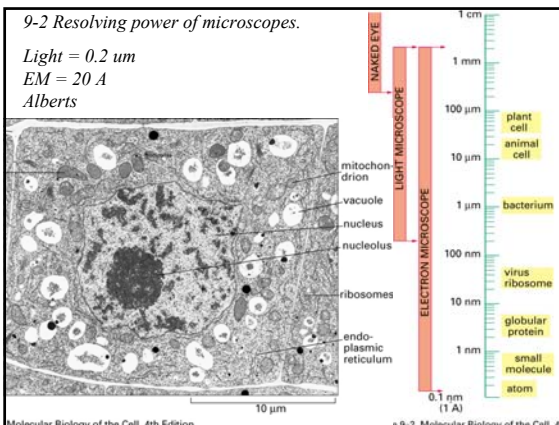
Read chapters to get an idea. Will see examples in
journal discussions.

9-2 Resolving power of microscopes.

Light = 0.2 μm

EM = 20 \AA

Alberts

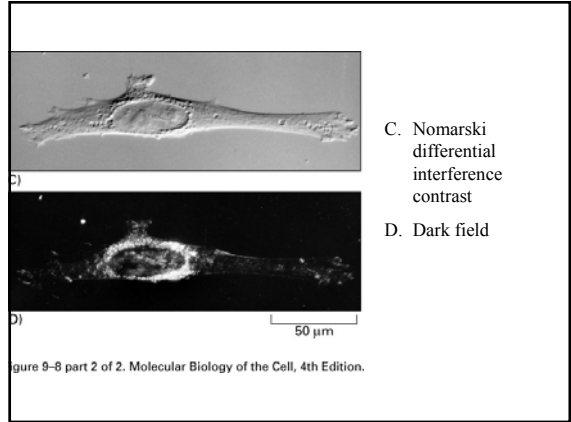
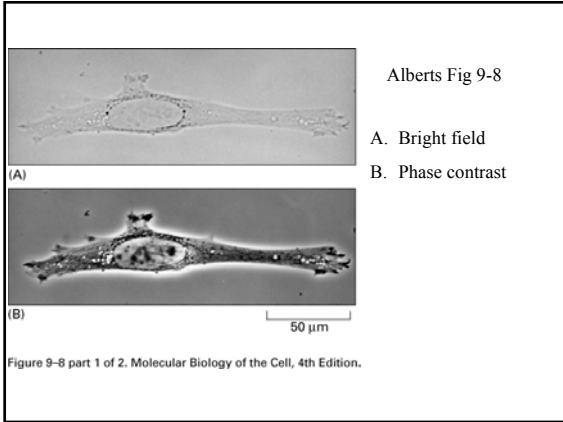


Light Microscopy

- Low resolution
- Can view dead and living cells
- Bright Field- fixed, sectioned, stained
- Fluorescence: fixed or living
- Phase contrast- living
- DIC or Nomarski- living
- Confocal fluorescence- 3D
- Image deconvolution- 3D
- Visualize location and/or movement of molecules in living cells

Electron Microscopy

- High resolution
- Detailed structure.
- Tissue- fixed, dead
 - sectioned
 - stained
- Specific molecules can be localized with gold-linked antibodies
- Rapid freeze cryo-EM



Observations raise many Questions:

What **molecules form the structures**?

What are the **functions** of the subcellular parts?

What **activities** do they have?

How do cells respond to stimuli?

How does a single cell develop into an organized multicellular organism?

What controls development?

How do you **approach** these questions?

- Biochemical- & Biophysical**
Find the essential and minimum players (e.g. **proteins**) responsible for the structure and activity.
- Molecular genetics**- Find the genes responsible for the structure, response. Mutate.
- Cell Biology**- Combine them to understand function in a cell and in an organism

Functional Genomics

How do we discover functions of genes?

Genetics
Biochemistry
Cell Biology

What is the role of a gene in a cell?
What role does it play in the whole organism?

Genes --> Proteins ---> Activities--> in cell

Methods used in Biochemical Approach:

- separate and purify an organelle or protein
- study its specific activity or role
- develop simple cell-free systems to determine the essential components required for activity.

How?

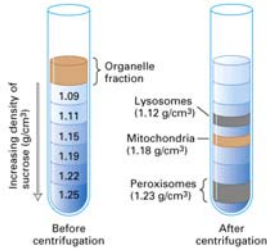
- Cell Fractionation**
- Centrifugation
- Column Chromatography
- Electrophoresis
- Reconstitute activity

5-47. Cell fractionation by differential centrifugation

Goal: separate, purify then measure activity

8-8 Alberts

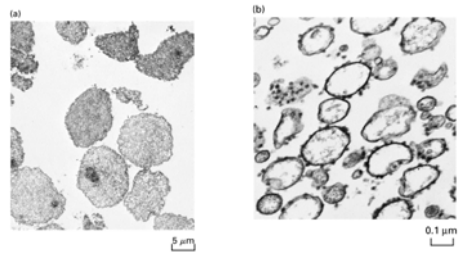
5-24. Separation of organelles by density gradient centrifugation



How do you verify if a fraction contains e.g. mitoch?

8-9 Alberts

5-25. EM of a) nuclei and b) ER purified from rat liver

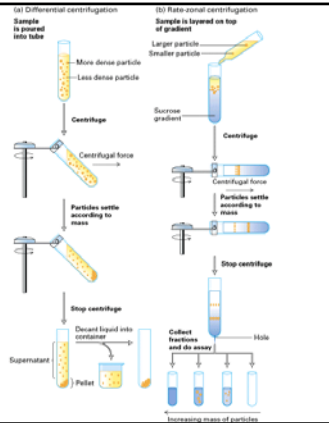


Goal- Verify purity of isolated fractions

- a. microscopy
- b. Biochemical enzyme activity [marker]
- c. Immunostaining with antibody to marker

3-40

Centrifugation to separate particles differing in mass or density



To get highly purified organelles, there are new methods :

Affinity methods

Antibody coated vesicles

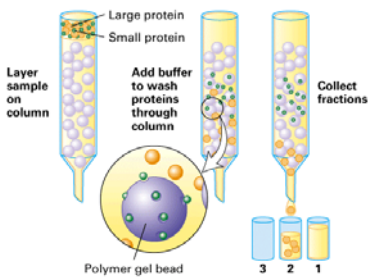
Physical methods

Phagosome containing low-density latex beads

How do you separate a mixture of proteins to find the one you want?

3-43. Column Chromatography to separate proteins in active form

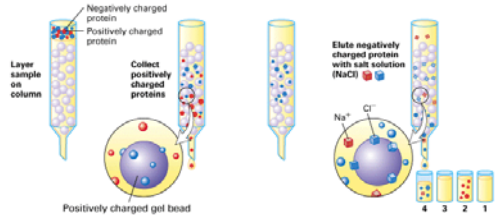
(a) Gel filtration chromatography Separate based on size



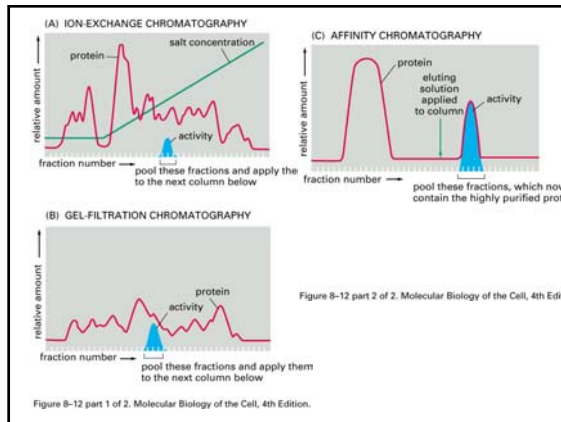
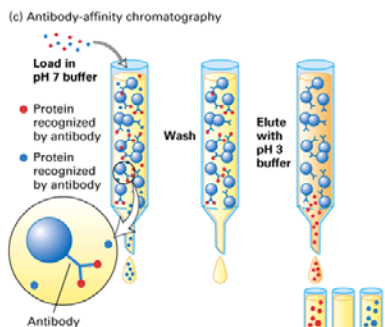
Separate based on charge

3-43

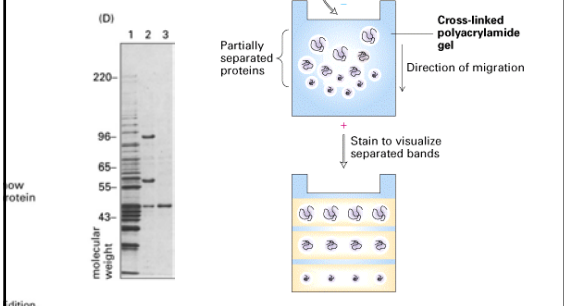
(b) Ion-exchange chromatography



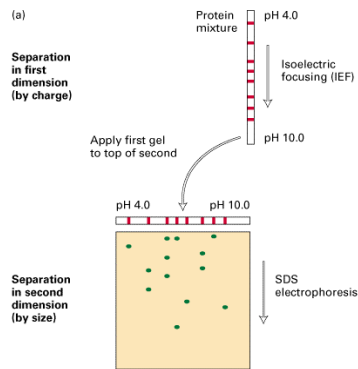
3-43c



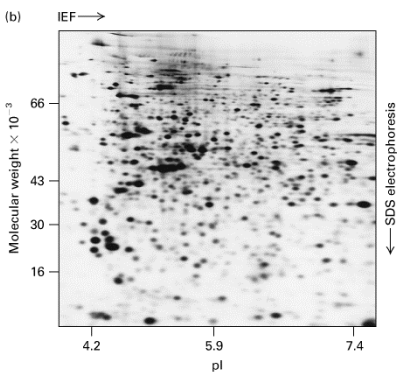
3-41. SDS polyacrylamide gel electrophoresis- to separate proteins of different masses



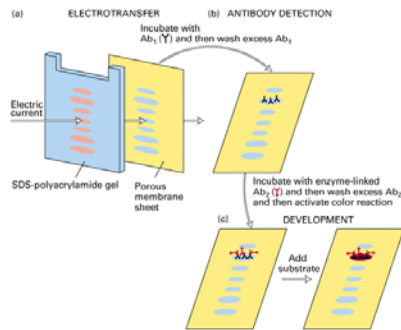
3-42. 2-D gel. A method to separate proteins based on different mass and charge.



3-42b



3-44. Western blot: using a specific antibody to recognize a specific protein. 2nd ab is linked to an enzyme that gives a colored product.



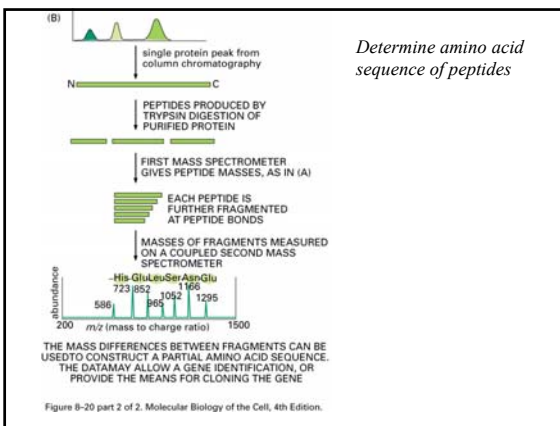
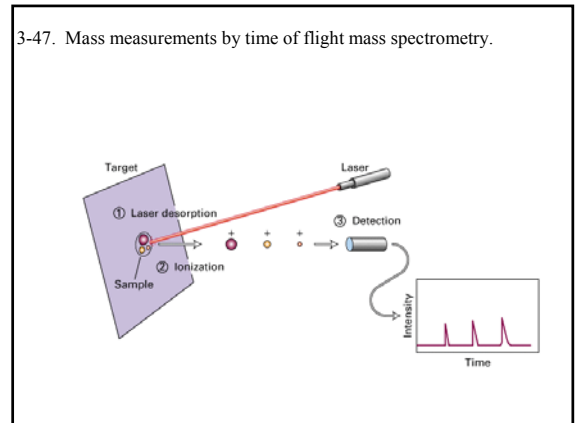
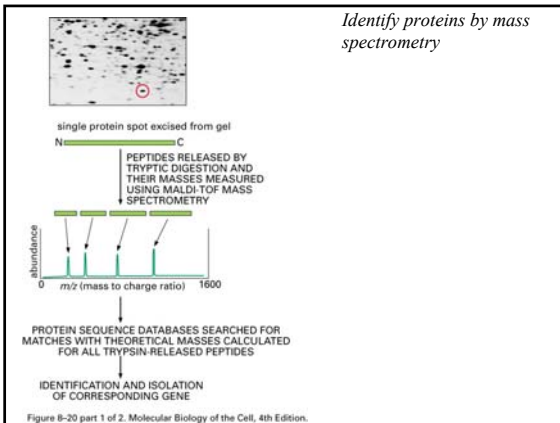
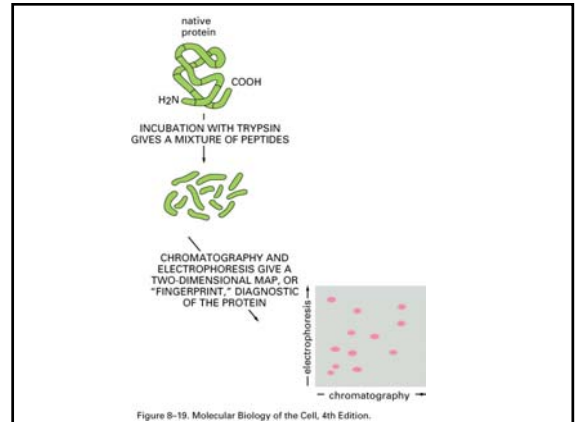
Cell biologists are now using organelle proteomics

to identify and localize all proteins in each organelle
Thus building a cell map.

Ref. Brunet et al M Desjardins 2003. Trends Cell Biol. 13, 629

Method:

1. Purify organelle or complex
2. Run 2-D gel
3. Cut out each protein spot
4. Digest with trypsin
5. Determine mass of peptides, characteristic for each protein.
6. Use protein database of sequenced genome to identify protein.



Cell Map. From: Brunet et al 2003 TiCB

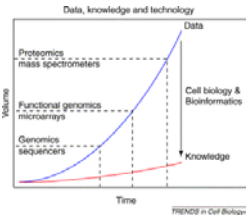
Phagosome -625 proteins <ul style="list-style-type: none"> • EB3-mediated phagocytosis • Lipid microdomains • Compartment for antigen cross presentation 	Nucleus 271 proteins <ul style="list-style-type: none"> • Confirmation of the localization of 18 new proteins • New compartment, perinuclear 	Spliceosome 292 proteins <ul style="list-style-type: none"> • Extensive work on protein mapping • Proteinic correlation between transcription and splicing 	
Exosome 49 proteins <ul style="list-style-type: none"> • Distinct to specific blebs • Inactivation of aminoacyl tRNA synthetase • Presence of γ-secretase 	Liposome 29 proteins <ul style="list-style-type: none"> • Identification of 3 novel lipoproteins • Presence of γ-secretase 	Spindle pole (Centrosome) 23 proteins <ul style="list-style-type: none"> • Identification of 18 novel components • New topological information 	Mitochondrion -613 proteins <ul style="list-style-type: none"> • 18 novel gene products • Linking cytochrome c to respiratory complexes III, IV • Respiratory complex formation independent of mtDNA
Cathrin-coated vesicle -250 proteins <ul style="list-style-type: none"> • Identification of 10 novel proteins • Ethipregnen stimulates catenin assembly 	Lipid raft 241 proteins <ul style="list-style-type: none"> • Authentication of raft proteins using BiAC • Lipid raft represent less than 10% of total lipids 	Golg -136 proteins <ul style="list-style-type: none"> • Activation of Pfaff and OGDH • Identification of GPP34 as a novel Golgi protein 	Nuclear pore 174 proteins <ul style="list-style-type: none"> • Identification and validation of 34 novel components • Novel model for nucleocytoplasmic transport

What are drawn
How can you prove if the proteins are actually on the said organelle?

FIGURE 2 Cell Map

Brunet et al 2003. *TiCB*

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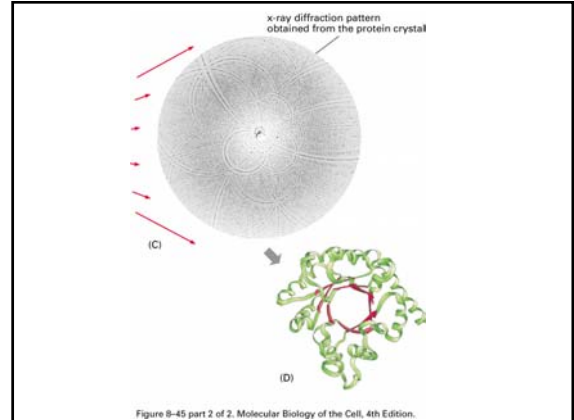


Figure 8-45 part 2 of 2. Molecular Biology of the Cell, 4th Edition.

Sequence similarity gives clues about protein function-
BLAST

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Score = 399 bits (1025), Expect = e-111
Identities = 198/290 (68%), Positives = 241/290 (82%), Gaps = 1/290

Query: 57  MEFQVEKIGGOTYGVVYKAKNKEVQVVALEKKIKLQTEEGVPTAIRISLLKELNE 116
           ME **KVEKIGGOTYGVVYKA *K * E *VALEKIRL* E EGVPSTAIRISILRE*HH
Sbjct: 1   MEFQVEKIGGOTYGVVYKAEKFKTKESTALEKKIKLQTEEGVPTAIRISILKRSNH 60

Query: 117  ENIVKLEDVITERKLYLVFEPFLHGDLEKFPMDASALGQIPELIKSYLFQLLGLAPCHS 176
           NIVPE DVVRE **ELVRE* ELKRPD* LKSLQVH QVAVCHS
Sbjct: 61  ENIVRLDQVHSEENIYLVFELDLEKFPMDSCPFAKNEPELIESLYQLLQVAVCHS 120

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Sbjct: 181 YSTVDVMSVGCIFAEVVKELFPDQSEIDELFKIPELGTPNQVMPQVSELDPFKEA 240

Query: 296  FFRWQDQVSRVYVPELDDQELLQNLHYDPNKRISAKALRHEFTQCV 345
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Sbjct: 241 FFRWQDQVSRVYVPELDDQELLQNLHYDPNKRISAKALRHEHYFKDL 290
    
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Figure 8-47. Molecular Biology of the Cell, 4th Edition.