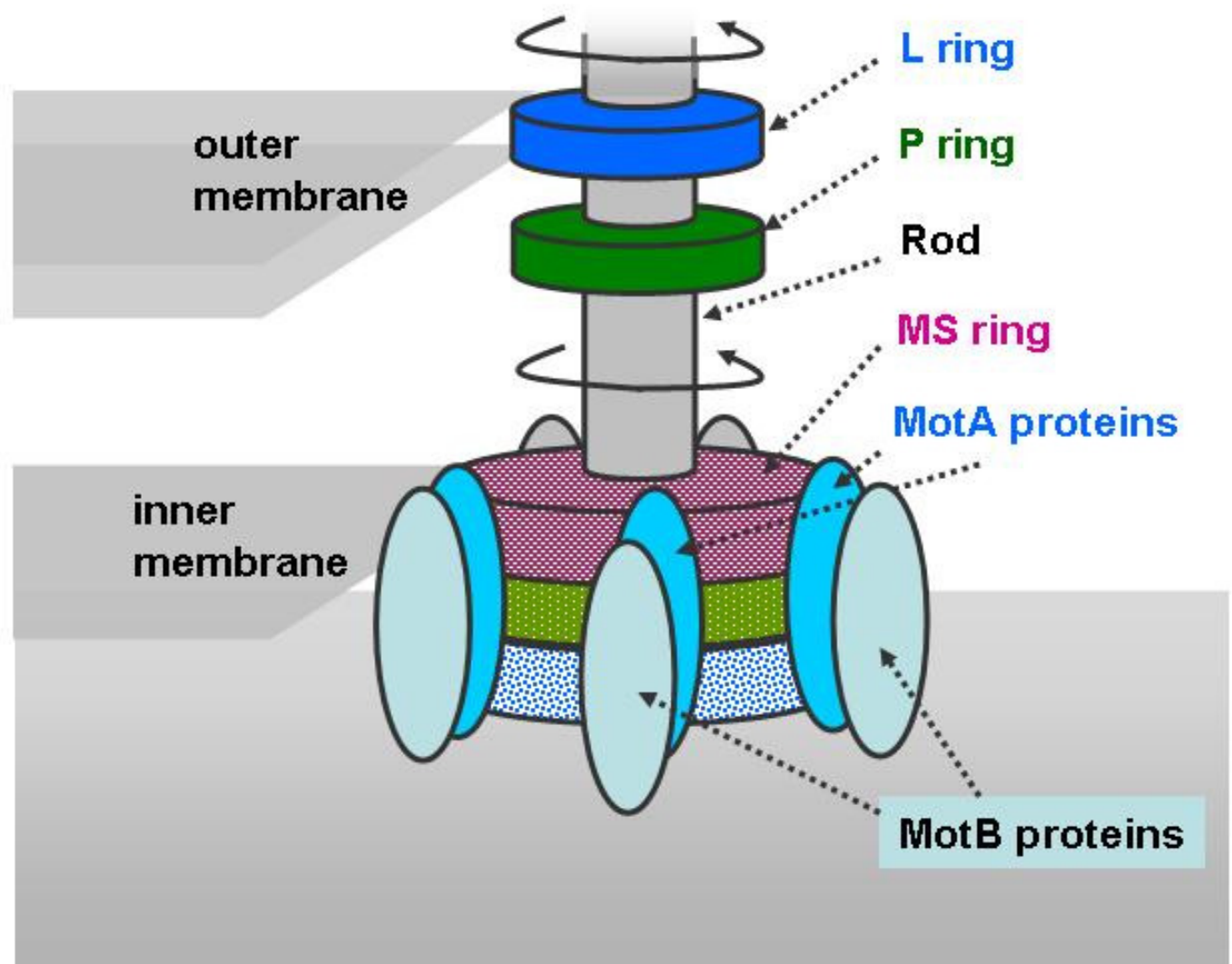


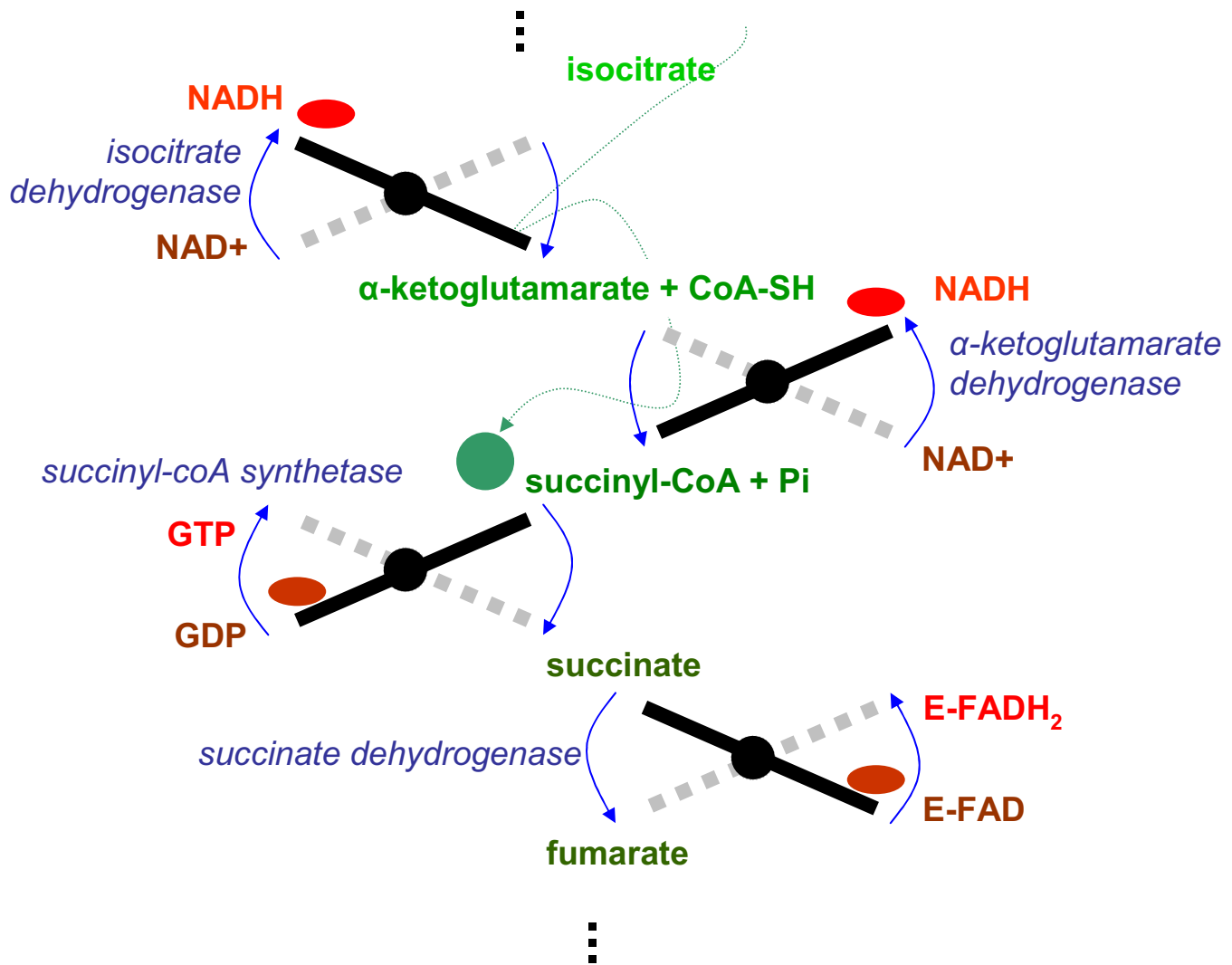
Figure 3: Internal Organization of a Eukaryotic Animal Cell



Structure of a bacterial flagellum (simplified). About 40 different proteins form this complex. The MS ring is made up of about 30 FliG subunits, and about 11 MotA/MotB protein pairs surround the MS ring. It is believed that these pairs, together with FliG, form an ion channel. As ions pass through the channel, conformational changes cause the MS ring to rotate, much like a waterwheel.

A similar “molecular motor” is used in ATP synthesis in a mitochondrion: rotation, driven by ions flowing through a channel, is the energy used to convert ADP to ATP. (See the section below, “Energy and Pathways”).

Figure 9: The Bacterial Flagellum (simplified)



Part of the TCA cycle (also called the citric acid cycle or the Krebs cycle) in action. A high-energy molecule of **isocitrate** has been converted to a lower-energy molecule called **α-ketoglutarate** and then to a still lower-energy molecule, **succinyl-CoA** (as shown by the path taken by the green circle). In the process two low-energy **NAD⁺** molecules have been converted to high-energy **NADH** molecules. Each “see-saw” is an enzyme (named in *italics*) that couples the two reactions. The next steps in the cycle will convert the **succinyl-CoA** to **succinate** and then **fumarate**, producing two more high-energy molecules, **GTP** and **E-FADH₂**.

Figure 17: Part of an Energy-Producing Pathway

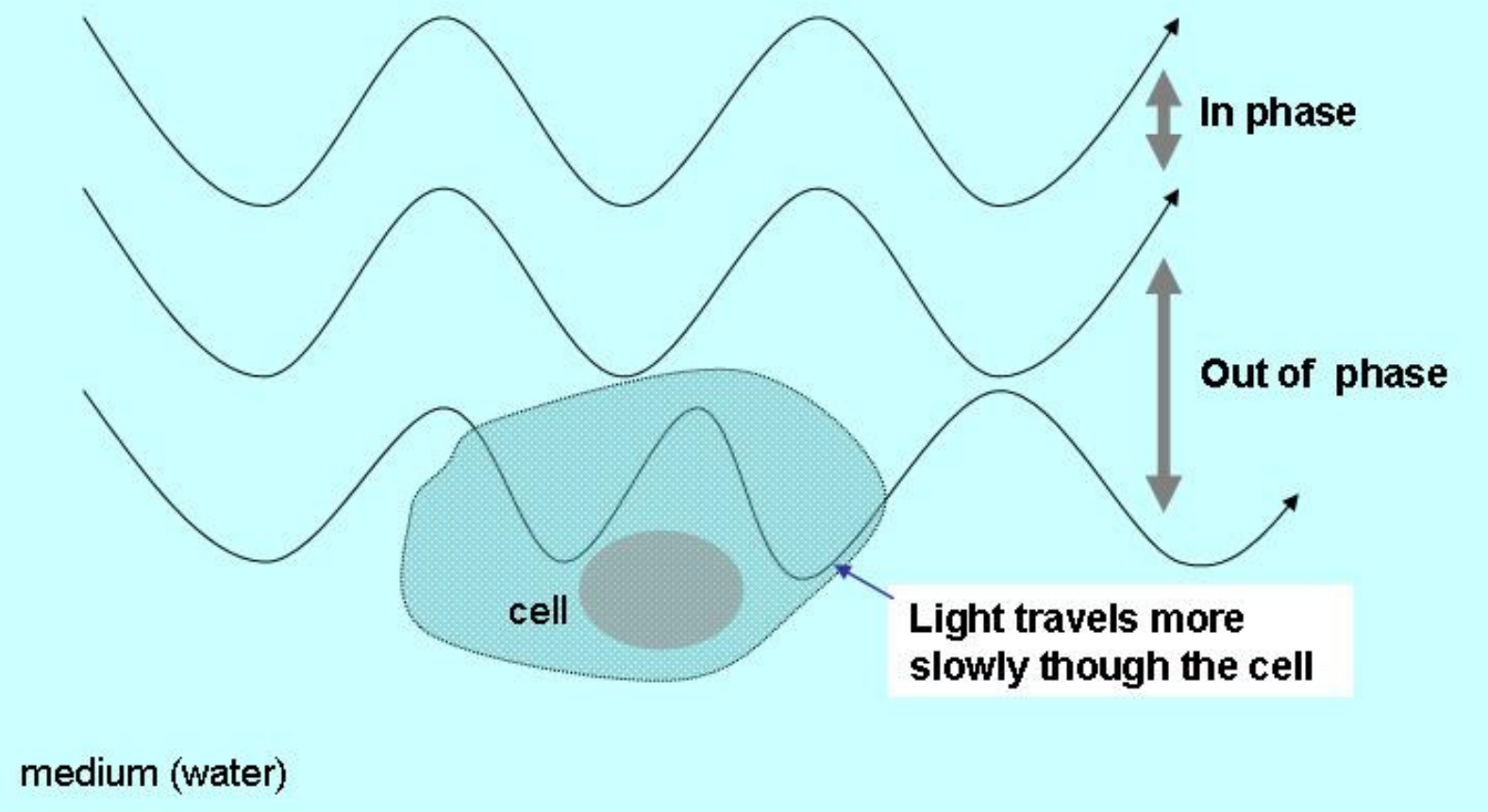
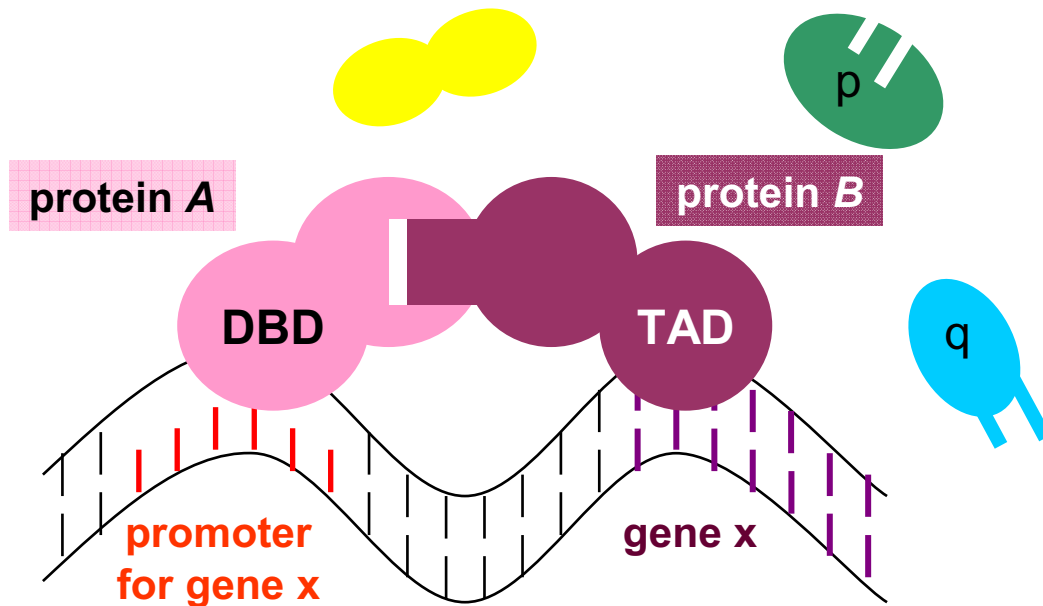


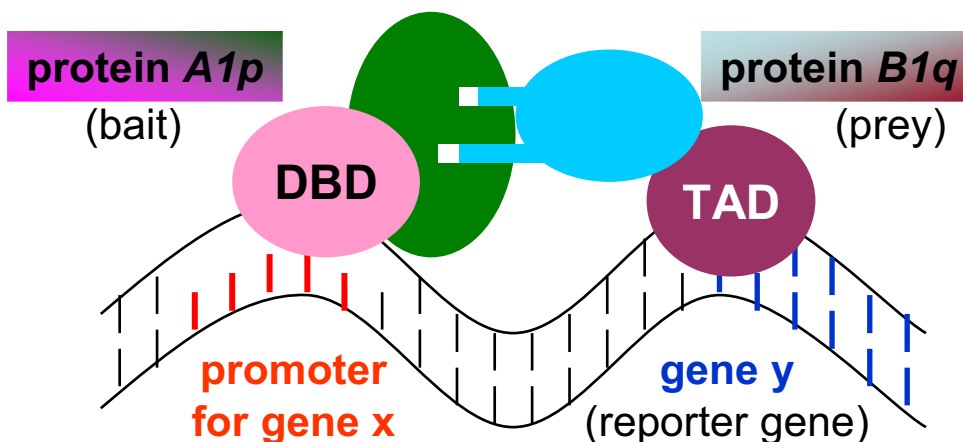
Figure 22: How A Differential Interference Contrast (DIC) Microscope Works

(A)



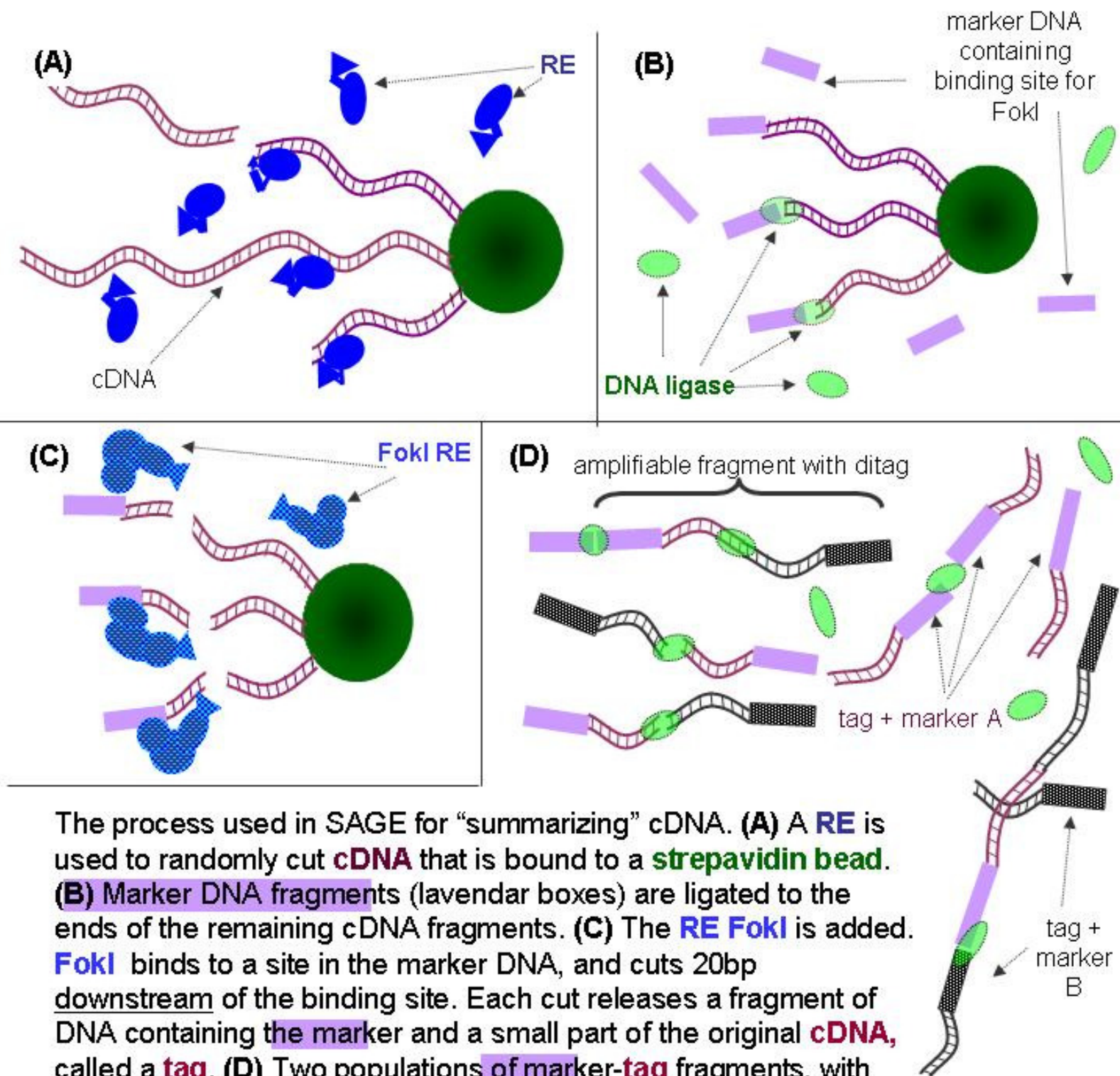
(A) In wild yeast, **A** binds **B**, which activates **gene x**. Only the DNA binding domain (DBD) is needed for **A** to find the promoter site, and only the transcription activation domain (**TAD**) is needed for **B** to activate transcription.

(B)



(B) In hybrid yeast, the DNA has a promoter for **x** near a **reporter gene y**. **A1p** can bind to the promoter site using the DBD of **A**, and **B1q** will activate transcription—of **gene y**—using the **TAD** of **x**. But **A1p** will only recruit **B1q** if proteins **p** and **q** bind. So, **y** is expressed iff **p** and **q** bind.

Figure 29. The yeast two-hybrid system



The process used in SAGE for “summarizing” cDNA. **(A)** A **RE** is used to randomly cut **cDNA** that is bound to a **strepavidin bead**. **(B)** Marker DNA fragments (lavender boxes) are ligated to the ends of the remaining cDNA fragments. **(C)** The **RE FokI** is added. **FokI** binds to a site in the marker DNA, and cuts 20bp downstream of the binding site. Each cut releases a fragment of DNA containing the **marker** and a small part of the original **cDNA**, called a **tag**. **(D)** Two populations of **marker-tag** fragments, with different markers, are mixed and ligated together. PCR can be used to amplify those cDNA fragments containing both markers, which must also contain at least two tags. These **ditag**-containing DNAs are then sequenced, revealing the sequence of the 20bp **tags** snipped off by the **FokI RE**.

Figure 33. Serial analysis of gene expression (SAGE)



<http://www.springer.com/978-0-387-48275-0>

A Computer Scientist's Guide to Cell Biology

Cohen, W.W.

2007, XIV, 100 p. 16 illus., Softcover

ISBN: 978-0-387-48275-0