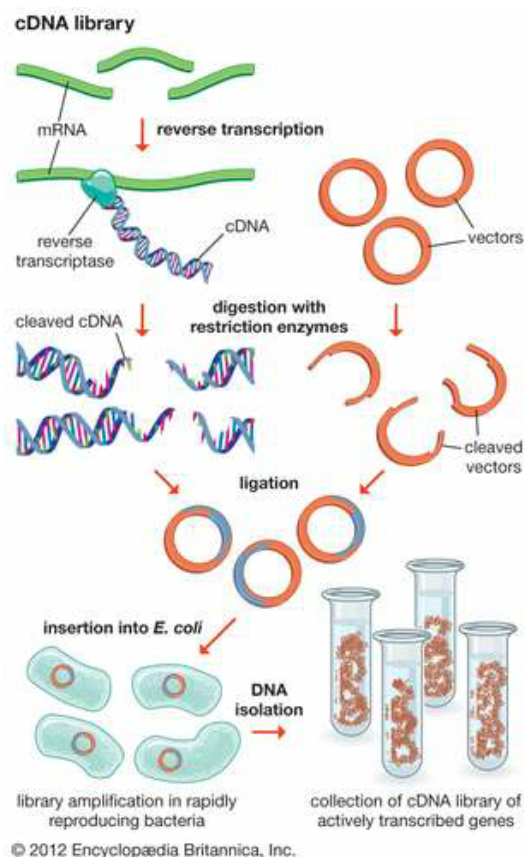


RESTRICTION ENZYME

KUMARI SONA RANI
ASSISTANT PROFESSOR
DEPARTMENT OF BOTANY
S.SINHA COLLEGE, AURANGABAD

FOR M.Sc 4TH SEMESTER STUDENTS

Restriction enzyme, also called **restriction endonuclease**, a [protein](#) produced by [bacteria](#) that [cleaves DNA](#) at specific sites along the [molecule](#). In the bacterial cell, restriction enzymes [cleave](#) foreign DNA, thus eliminating infecting organisms. Restriction enzymes can be isolated from bacterial cells and used in the laboratory to manipulate fragments of DNA, such as those that contain [genes](#); for this reason they are indispensable tools of [recombinant DNA technology](#) ([genetic engineering](#)).



cDNA libraryA

A bacterium uses a restriction [enzyme](#) to defend against bacterial viruses called [bacteriophages](#), or phages. When a phage infects a bacterium, it inserts its DNA into the

bacterial cell so that it might be replicated. The restriction enzyme prevents replication of the phage DNA by cutting it into many pieces. Restriction enzymes were named for their ability to restrict, or limit, the number of strains of bacteriophage that can infect a bacterium.

Each restriction enzyme recognizes a short, specific sequence of [nucleotide](#) bases (the four basic chemical subunits of the linear double-stranded DNA molecule—[adenine](#), [cytosine](#), [thymine](#), and [guanine](#)). These regions are called recognition sequences, or recognition sites, and are randomly distributed throughout the DNA. Different bacterial [species](#) make restriction enzymes that recognize different nucleotide sequences.

When a restriction endonuclease recognizes a sequence, it snips through the DNA molecule by catalyzing the [hydrolysis](#) (splitting of a chemical bond by addition of a water molecule) of the bond between [adjacent](#) nucleotides. Bacteria prevent their own DNA from being degraded in this manner by disguising their recognition sequences. Enzymes called methylases add [methyl groups](#) ($-CH_3$) to adenine or cytosine bases within the recognition sequence, which is thus modified and protected from the endonuclease. The restriction enzyme and its corresponding methylase [constitute](#) the restriction-modification system of a bacterial species. Traditionally, four types of restriction enzymes are recognized, designated I, II, III, and IV, which differ primarily in structure, cleavage site, specificity, and cofactors. Types I and III enzymes are similar in that both restriction and methylase activities are carried out by one large enzyme complex, in contrast to the type II system, in which the restriction enzyme is independent of its methylase. [Type II restriction enzymes](#) also differ from types I and III in that they cleave DNA at specific sites within the recognition site; the others cleave DNA randomly, sometimes hundreds of bases from the recognition sequence. Several thousand type II restriction enzymes have been identified from a variety of bacterial species. These enzymes recognize a few hundred distinct sequences, generally four to eight bases in length. Type IV restriction enzymes cleave only methylated DNA and show weak sequence specificity. Restriction enzymes were discovered and characterized in the late 1960s and early 1970s by molecular biologists [Werner Arber](#), [Hamilton O. Smith](#), and [Daniel Nathans](#). The ability of the enzymes to cut DNA at precise locations enabled researchers to isolate gene-containing fragments and recombine them with other molecules of DNA—i.e., to [clone](#) genes. The names of restriction enzymes are derived from the [genus](#), species, and strain [designations](#) of the bacteria that produce them; for example, the enzyme *EcoRI* is produced by *Escherichia coli* strain RY13. It is thought that restriction enzymes originated from a common ancestral protein and evolved to recognize specific sequences through processes such as genetic recombination and gene amplification.