Hind 2 Recognition Sequence

== History == 1b6128615d 3'-T T C G A| A-5' 1b6128615d

Dear enemy effect Some authors have suggested the dear enemy effect is territory residents displaying lower levels of aggression toward familiar neighbours compared to unfamiliar individuals who are non-territorial "floaters". As territory owners become accustomed to their neighbours, they expend less time and energy on defensive behaviors directed toward one another. The dear enemy effect or dear enemy recognition is an ethological phenomenon in which two neighbouring territorial animals become less aggressive toward The dear enemy effect or dear enemy recognition is an ethological phenomenon in which two neighbouring territorial animals become less aggressive toward one another once territorial borders are well established. However, aggression toward unfamiliar neighbours remains the same 1b6128615d

The effect is the converse of the nasty neighbour effect, in which some species are more aggressive towards their neighbours than towards unfamiliar strangers. 1b6128615d

HaeIII aegyptius bacteria. HaeIII is not effective for single stranded DNA cleavage. This enzyme's gene has been sequenced and cloned. This is done to make DNA fragments in blunt ends. It is a restriction enzyme used in molecular biology laboratories. The enzyme's recognition site—the place where it cuts DNA molecules—is the GGCC nucleotide sequence which means it cleaves DNA at the site 5′-GG/CC-3. It was the third endonuclease to be isolated from the Haemophilus aegyptius bacteria. The enzyme's recognition site—the place where it cuts DNA molecules—is the GGCC nucleotide sequence which means it cleaves DNA at the HaeIII is one of many restriction enzymes (endonucleases) a type of prokaryotic DNA that protects organisms from unknown, foreign DNA. The recognition site is usually around 4-8 bps 1b6128615d

== Function == 1b6128615d

Nuclease Nucleases are also extensively used in molecular cloning. within a specific sequence of six base pairs. Defects in certain nucleases can cause genetic instability or immunodeficiency. They found that the HindII enzyme

always cuts directly in the center of this sequence (between the 3rd and In biochemistry, a nuclease (also archaically known as nucleodepolymerase or polynucleotidase) is an enzyme capable of cleaving the phosphodiester bonds that link nucleotides together to form nucleic acids. Nucleases variously affect single and double stranded breaks in their target molecules. In living organisms, they are essential machinery for many aspects of DNA repair 1b6128615d

There are two primary classifications based on the locus of activity. Exonucleases digest nucleic acids from the ends. Endonucleases act on regions in the middle of target molecules. They are further subcategorized as deoxyribonucleases and ribonucleases. The former acts on DNA, the latter on RNA. 1b6128615d Source: Organism that naturally produces the enzyme. 1b6128615d == Overview == 1b6128615d

Promoter (genetics) In genetics, a promoter is a sequence of DNA to which proteins bind to initiate transcription of a single RNA transcript from the DNA downstream of the In genetics, a promoter is a sequence of DNA to which proteins bind to initiate transcription of a single RNA transcript from the DNA downstream of the promoter. Promoters are located near the transcription start sites of genes, upstream on the DNA (towards the 5' region of the sense strand). The RNA transcript may encode a protein (mRNA), or can have a function in and of itself, such as tRNA or rRNA 1b6128615d

The following information is given: 1b6128615d Cut: Cutting site and DNA products of the cut. The recognition sequence and the cutting site usually match, but sometimes the cutting site can be dozens of nucleotides away from the recognition site. 1b6128615d == Properties == 1b6128615d The dear enemy effect has been observed in a wide range of animals including mammals, birds, reptiles, amphibians, fish and invertebrates. It can be modulated by factors such as the location of the familiar and unfamiliar animal, the season, and the presence of females. 1b6128615d For transcription to take place, the enzyme that synthesizes RNA, known as RNA polymerase, must attach to the DNA near a gene. Promoters contain specific DNA sequences such as response elements that provide a secure initial binding site for RNA polymerase and for proteins called transcription factors that recruit RNA polymerase. These transcription factors have specific activator or repressor sequences of corresponding nucleotides that attach to specific promoters and regulate gene expression. 1b6128615d In the late 1960s, scientists Stuart Linn and Werner Arber isolated examples of the two types of enzymes responsible for phage growth restriction in Escherichia coli

(E. coli) bacteria. One of these enzymes added a methyl group to the DNA, generating methylated DNA, while the other cleaved unmethylated DNA at a wide variety of locations along the length of the molecule.... 1b6128615d

List of restriction enzyme cutting sites: G–K action. Recognition sequence: Sequence of DNA recognized by the enzyme and to which it specifically This article contains a list of the most studied restriction enzymes whose names start with G to K inclusive. Source: Organism that naturally produces the enzyme. It contains approximately 90 enzymes 1b6128615d

The classical restriction enzymes cut up, and hence render harmless, any unknown (non-cellular) DNA that enters a bacterial cell as a result of a viral infection. They recognize a specific DNA sequence, usually short (3 to 8 bp), and cut it, producing either blunt or overhung ends, either at or nearby the recognition site. 1b6128615d == Restriction enzymes catalog == 1b6128615d The ultimate function of the dear enemy effect is to increase the individual fitness of the animal expressing the behaviour... 1b6128615d == "Repeats" in proteins == 1b6128615d Isoschizomers and neoschizomers: An isoschizomer is an enzyme that recognizes the same sequence as another. A neoschizomer is a special type of isoschizomer that recognizes the same sequence as another, but cuts... 1b6128615d Promoters can be about 100–1000 base pairs long, the sequence of which is highly dependent on the gene and product of transcription, type or class of RNA polymerase recruited to the site, and species of organism. 1b6128615d

Endonuclease Endonucleases differ from exonucleases, which cleave the ends of recognition sequences instead of the middle (endo) portion. Evidence suggests that endonuclease activity experiences a lag compared to exonuclease activity. Type III, however, cleaves the DNA at about 25 base pairs from the recognition sequence and also requires ATP In molecular biology, endonucleases are enzymes that cleave the phosphodiester bond within a polynucleotide chain (namely DNA or RNA). Some, such as deoxyribonuclease I, cut DNA relatively nonspecifically (with regard to sequence), while many, typically called restriction endonucleases or restriction enzymes, cleave only at very specific nucleotide sequences. BamHI, EcoRI, EcoRV, HindIII, and HaeIII. Some enzymes known as "exo-endonucleases", however, are not limited to either nuclease function, displaying qualities that are both endo- and exo-like 1b6128615d

HaeIII has a molecular weight of 37126. After a 2-10-fold of HaeIII takes place, there is overdigestion of a DNA substrate. This results in 100% being cut, more than 50% of fragments being ligated, and more than 95% being

recut. Heat inactivation comes at about 80 °C for 20 minutes. The locus of the HaeIII enzyme is on AF05137, and is linear with 957 base pairs. 1b6128615d Restriction endonucleases are used as defense mechanisms in prokaryotic organisms in the restriction modification system. Their primary function is to protect the host genome against invasion by foreign DNA, primarily bacteriophage DNA. There is also evidence that suggests the restriction enzymes may act alongside modification enzymes as selfish elements, or may be involved in genetic recombination and transposition. 1b6128615d

Protein tandem repeats Repetitive units of protein tandem repeats are considerably diverse, ranging from the repetition of a single amino acid to domains of 100 or more residues. or similar sequence motifs. These periodic sequences are generated by internal duplications in both coding and non-coding genomic sequences. These periodic sequences are generated by internal duplications in both coding and non-coding genomic sequences. Repetitive An array of protein tandem repeats is defined as several (at least two) adjacent copies having the same or similar sequence motifs 1b6128615d

Recognition sequence: Sequence of DNA recognized by the enzyme and to which it specifically binds. 1b6128615d Restriction enzymes are quite variable in the short DNA sequences they recognize. An organism often has several different enzymes, each specific to a distinct short DNA sequence. 1b6128615d

Restriction enzyme e. each strand) of the DNA double helix. In 1970, Hamilton O. Smith, Thomas Kelly and Kent Wilcox isolated and characterized the first type II restriction enzyme, HindII, A restriction enzyme, restriction endonuclease, REase, ENase or restrictase is an enzyme that cleaves DNA into fragments at or near specific recognition sites within molecules known as restriction sites. Restriction enzymes are commonly classified into five types, which differ in their structure and whether they cut their DNA substrate at their recognition site, or if the recognition and cleavage sites are separate from one another. Restriction enzymes are one class of the broader endonuclease group of enzymes. the recognition site. To cut DNA, all restriction enzymes make two incisions, once through each sugar-phosphate backbone (i 1b6128615d

More than 3,600 restriction endonucleases are known which represent over 250 different specificities. Over... 1b6128615d The list includes some of the most studied examples of restriction endoncleases. The following information

is given: 1b6128615d

List of restriction enzyme cutting sites specific DNA sequence, usually short (3 to 8 bp), and cut it, producing either blunt or overhung ends, either at or nearby the recognition site. Restriction A restriction enzyme or restriction endonuclease is a special type of biological macromolecule that functions as part of the "immune system" in bacteria. One special kind of restriction enzymes is the class of "homing endonucleases", these being present in all three domains of life, although their function seems to be very different from one domain to another 1b6128615d

Enzyme: Accepted name of the molecule, according to the internationally adopted nomenclature, and bibliographical references. (Further reading: see the section "Nomenclature" in the article "Restriction enzyme".) 1b6128615d These enzymes are found in bacteria and archaea and provide a defense mechanism against invading viruses. Inside a prokaryote, the restriction enzymes selectively cut up foreign DNA in a process called restriction digestion; meanwhile, host DNA is protected by a modification enzyme (a methyltransferase) that modifies the prokaryotic DNA and blocks cleavage. Together, these two processes form the restriction modification system. 1b6128615d PDB code: Code used to identify the structure of a protein in the PDB database of protein structures. The 3D atomic structure of a protein provides highly valuable information to understand the intimate details of its mechanism of action. 1b6128615d The cleavage of this sequence between the AA's results in 5' overhangs on the DNA called sticky ends: 1b6128615d Restriction enzymes are endonucleases from eubacteria and archaea that recognize a specific DNA sequence. The nucleotide sequence recognized for cleavage by a restriction enzyme is called the restriction site. Typically, a restriction site will be a palindromic sequence about four to six nucleotides long. Most restriction endonucleases cleave the DNA strand unevenly, leaving complementary single-stranded ends. These ends can reconnect through hybridization and... 1b6128615d 5'-A |A G C T T-3' 1b6128615d

HindIII mechanism of DNA recognition and phosphodiester bond cleavage. However, it is believed that HindIII utilizes a common mechanism of recognition and catalysis HindIII (pronounced "Hin D Three") is a type II site-specific deoxyribonuclease restriction enzyme isolated from Haemophilus influenzae that cleaves the DNA palindromic sequence AAGCTT in the presence of the cofactor Mg2+ via hydrolysis 1b6128615d

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