DOWNLOAD PDF DNA RECOGNITION IN PROCARYOTES BY HELIX-TURN-HELIX MOTIFS

Chapter 1 : Protein Motifs: the Helixâ€•Turnâ€•Helix Motif

DNA Recognition in Prokaryotes by Helix-Turn-Helix Motifs 1. Helix-turn-helix proteins 2. Zinc finger proteins the helix-turn-helix motif in DNA binding protein.

Protein - DNA Interaction: General Nucleic acids are the storage of genetic information and this information has to be accessible and inherited. Nucleic acids need proteins for storage, replication, and transcription purposes. The specificity of the transcription and replication requires recognition on the molecular level between protein structures and nucleic acid structures. The genetic code has to be readable. The reading of the code is a conformationally specific interaction between amino acids and nucleic acids. Surface properties of the macromolecules involved are the essential key in the recognition process. Electrostatic interaction, hydrogen bonding capability and hydrophobic effects are of importance. Complementarity in surface profiles is the essential mechanism that provides the specificity. Here we discuss a few selected protein systems that recognize DNA double helical structures. The sequence of the base pairs in the double helix specifies the local conformation of the double helix - its ribose-phosphate backbone and the dimensions of the minor and major grooves of the helix. Proteins that bind DNA and are involved in replication or transcription do so in a sequence specific way. Transcription factors are dimers when active, i. Dimerization is a regulatory mechanism of controlling transcription factor activity. There are 3 common features most DNA binding proteins have in common: The motif resembles that of an EF hand described in calmodulin. The F-helix is the recognition helix and the side chains give the specificity of binding. Sometimes more than one protein compete for the same sequence. As examples serve bacteriophages l , P22, and , where repressors and activators affect transcription. They can recognize the same DNA fragment. They have different binding interaction visualized by the two close, but not identical structures as determined by X-ray crystallography. They differ in their affinity for the same sequence, or DNA conformation, respectively through H-bonds, salt bridges and Van der Waals interactions. The relative concentrations of all proteins, therefore, determine which one is bound to the binding element most of the time, which in turn affects polymerase binding to the DNA determining if and in which direction transcription will occur. The ratio of all DNA binding proteins therefore determines the rate of transcription controlled by the DNA sequences in question. Leucine-zipper Eukaryotic transcription factors In some transcription factors the dimer binding site with the DNA forms a so called leucine zipper. The leucine zipper is a interdigitation of regularly spaced leucine residues in one helix with leucines from the adjacent helix. Mostly the helices involved in leucine zippers exhibit a heptad sequence abcdefg with residues a and d being hydrophobic and all others hydrophilic. Leucine zipper motifs can mediate either homo- or heterodimer formation. Note that the leucine zipper motif itself is not the DNA binding part of the helices. Helical wheel representation of heptad sequence found in leucine zipper motif Heptad sequence a to g has a Leu at position d and Met, Val, or Asn at position a enabling a hydrophobic interaction at the helix-helix interface. Each Zn-finger interacts in a conformationally identical manner with successive triple base pair segments in the major groove of the double helix. The protein-DNA interaction is determined by two factors: Zn-finger peptide undergoes folding transition upon metal binding Spheres at either end of peptide are fluorescence markers that are used to monitor folding fluorescence-resonance-energy transfer. They participate in transcription by all three nuclear RNA polymerases S. Burley, acting as subunit in each of them. The structure of TBP was solved at 2. The binding side is lined with the central 8 strands of the stranded anti-parallel b -sheet. The upper surface contains four a -helices and binds to various components of the transcription machinery. To view this structure use protein database accession number 1YTB. Burley, Crystal structures of TBP with bound double helical segments of viral promoter regions demonstrate an induced-fit mechanism of protein-DNA recognition. The bending of the double helix is mediate by the curved, 8 stranded b -sheet motif providing a large concave surface for minor groove and phosphate-ribose contacts with the 8 base pair TATA element S.

Chapter 2 : Kinemages and Kinemage Documentation

The common motifs include the helix-turn-helix, the homeodomain, the leucine zipper, the helix-loop-helix, and zinc fingers of several types. The precise amino acid sequence that is folded into a motif determines the particular DNA sequence that is recognized.

Click on the image to see a larger version. Selected References These references are in PubMed. This may not be the complete list of references from this article. Abel T, Maniatis T. Action of leucine zippers. Rhizobium meliloti nifN fixF gene is part of an operon regulated by a nifA-dependent promoter and codes for a polypeptide homologous to the nifK gene product. Nucleotide sequence of wild-type and mutant nifR4 ntrA genes of Rhodobacter capsulatus: The nif promoters of Klebsiella pneumoniae have a characteristic primary structure. Activator-independent formation of a closed complex between sigma holoenzyme and nifH and nifU promoters of Klebsiella pneumoniae. Specific binding of the transcription factor sigma to promoter DNA. Recognition of nucleotide sequences at the Escherichia coli galactose operon P1 promoter by RNA polymerase. Cassette mutagenesis implicates a helix-turn-helix motif in promoter recognition by the novel RNA polymerase sigma factor sigma Two amino acids in an RNA polymerase sigma factor involved in the recognition of adjacent base pairs in the region of a cognate promoter. A mutant Escherichia coli sigma 70 subunit of RNA polymerase with altered promoter specificity. A structural taxonomy of DNA-binding domains. DNA recognition by proteins with the helix-turn-helix motif. Structure and function of bacterial sigma factors. Products of nitrogen regulatory genes ntrA and ntrC of enteric bacteria activate glnA transcription in vitro: Transcription of glnA by purified Escherichia coli components: Constitutive function of a positively regulated promoter reveals new sequences essential for activity. Crystal structure of an engrailed homeodomain-DNA complex at 2. Expression of sigma 54 ntrA -dependent genes is probably united by a common mechanism. A general method for rapid site-directed mutagenesis using the polymerase chain reaction. The sigma 70 family: Cascades of Sigma factors. The nucleotide sequence of the sigma factor gene ntrA rpoN of Azotobacter vinelandii: The nucleotide sequence of the nitrogen-regulation gene ntrA of Klebsiella pneumoniae and comparison with conserved features in bacterial RNA polymerase sigma factors. Transcriptional activation of the Klebsiella pneumoniae nifLA promoter by NTRC is face-of-the-helix dependent and the activator stabilizes the interaction of sigma RNA polymerase with the promoter. In vivo studies on the interaction of RNA polymerase-sigma 54 with the Klebsiella pneumoniae and Rhizobium meliloti nifH promoters. The role of NifA in the formation of an open promoter complex. Two transcriptional start sites found in the promoter region of Escherichia coli glutamine permease operon, glnHPQ. Conserved residues make similar contacts in two repressor-operator complexes. Function of a bacterial activator protein that binds to transcriptional enhancers. A functional multigene family in Rhizobium phaseoli. Mutations that create new promoters suppress the sigma 54 dependence of glnA transcription in Escherichia coli. The regulation of transcription initiation in bacteria. Probing the Escherichia coli glnALG upstream activation mechanism in vivo. Role of eukaryotic-type functional domains found in the prokaryotic enhancer receptor factor sigma Altered promoter recognition by mutant forms of the sigma 70 subunit of Escherichia coli RNA polymerase. Scissors-grip model for DNA recognition by a family of leucine zipper proteins. Changes in conserved region 2 of Escherichia coli sigma 70 affecting promoter recognition. Stress-induced expression of the Escherichia coli phage shock protein operon is dependent on sigma 54 and modulated by positive and negative feedback mechanisms. Mutation changing the specificity of an RNA polymerase sigma factor.

Chapter 3 : COMET: Protein S/F- DNA Binders

seen in a number of prokaryotic and eukaryotic regulatory proteins and analyzes the way in which they recognize cognate DNA-binding sites (for other reviews, see).

CAP is a gene regulatory protein from E. In the absence of the bound protein, this DNA helix is straight. Particular nucleotide sequences, each typically less than 20 nucleotide pairs in length, function as fundamental components of genetic switches by serving as recognition sites for the binding of specific gene regulatory proteins. Thousands of such DNA sequences have been identified, each recognized by a different gene regulatory protein or by a set of related gene regulatory proteins. Some of the gene regulatory proteins that are discussed in the course of this chapter are listed in Table , along with the DNA sequences that they recognize. We now turn to the gene regulatory proteins themselves, the second fundamental component of genetic switches. We begin with the structural features that allows these proteins to recognize short, specific DNA sequences contained in a much longer double helix. Gene Regulatory Proteins Contain Structural Motifs That Can Read DNA Sequences Molecular recognition in biology generally relies on an exact fit between the surfaces of two molecules, and the study of gene regulatory proteins has provided some of the clearest examples of this principle. A gene regulatory protein recognizes a specific DNA sequence because the surface of the protein is extensively complementary to the special surface features of the double helix in that region. In most cases the protein makes a large number of contacts with the DNA, involving hydrogen bonds, ionic bonds, and hydrophobic interactions. Although each individual contact is weak, the 20 or so contacts that are typically formed at the protein-DNA interface add together to ensure that the interaction is both highly specific and very strong Figure In fact, DNA-protein interactions include some of the tightest and most specific molecular interactions known in biology. Figure The binding of a gene regulatory protein to the major groove of DNA. Only a single contact is shown. Typically, the protein-DNA interface would consist of 10 to 20 such contacts, involving different amino acids, each contributing to the strength of the more Although each example of protein - DNA recognition is unique in detail, x-ray crystallographic and NMR spectroscopic studies of several hundred gene regulatory proteins have revealed that many of the proteins contain one or another of a small set of DNA-binding structural motifs. The fit is so good that it has been suggested that the dimensions of the basic structural units of nucleic acids and proteins evolved together to permit these molecules to interlock. Originally identified in bacterial proteins, this motif has since been found in hundreds of DNA-binding proteins from both eucaryotes and procaryotes. The two helices are held at a fixed angle, primarily through interactions between the two helices. The more C-terminal helix is called the recognition helix because it fits into the major groove of DNA; its amino acid side chains, which differ from protein to protein, play an important part in recognizing the specific DNA sequence to which the protein binds. Figure The DNA-binding helix-turn-helix motif. The motif is shown in A , where each white circle denotes the central carbon of an amino acid. Outside the helix-turn-helix region, the structure of the various proteins that contain this motif can vary enormously Figure Moreover, in most of these proteins, parts of the polypeptide chain outside the helix-turn-helix domain also make important contacts with the DNA, helping to fine-tune the interaction. Figure Some helix-turn-helix DNA-binding proteins. All of the proteins bind DNA as dimers in which the two copies of the recognition helix red cylinder are separated by exactly one turn of the DNA helix 3. The other helix of the helix-turn-helix motif more The group of helix-turn-helix proteins shown in Figure demonstrates a feature that is common to many sequence-specific DNA -binding proteins. This arrangement allows each protein monomer to make a nearly identical set of contacts and enormously increases the binding affinity: The nucleotides labeled in green in this sequence are arranged symmetrically, allowing each half of the DNA site to be recognized in the same way by each protein monomer, also more Homeodomain Proteins Constitute a Special Class of Helix-Turn-Helix Proteins Not long after the first gene regulatory proteins were discovered in bacteria, genetic analyses in the fruit fly Drosophila led to the characterization of an important

class of genes, the homeotic selector genes, that play a critical part in orchestrating fly development. As discussed in Chapter 21, they have since proved to have a fundamental role in the development of higher animals as well. Mutations in these genes cause one body part in the fly to be converted into another, showing that the proteins they encode control critical developmental decisions. When the nucleotide sequences of several homeotic selector genes were determined in the early s, each proved to contain an almost identical stretch of 60 amino acids that defines this class of proteins and is termed the homeodomain. When the three-dimensional structure of the homeodomain was determined, it was seen to contain a helix-turn-helix motif related to that of the bacterial gene regulatory proteins, providing one of the first indications that the principles of gene regulation established in bacteria are relevant to higher organisms as well. More than 60 homeodomain proteins have now been discovered in Drosophila alone, and homeodomain proteins have been identified in virtually all eucaryotic organisms that have been studied, from yeasts to plants to humans. The structure of a homeodomain bound to its specific DNA sequence is shown in Figure Whereas the helix-turn-helix motif of bacterial gene regulatory proteins is often embedded in different structural contexts, the helix-turn-helix motif of homeodomains is always surrounded by the same structure which forms the rest of the homeodomain , suggesting that the motif is always presented to DNA in the same way. Indeed, structural studies have shown that a yeast homeodomain protein and a Drosophila homeodomain protein have very similar conformations and recognize DNA in almost exactly the same manner, although they are identical at only 17 of 60 amino acid positions see Figure A homeodomain bound to its specific DNA sequence. Two different views of the same structure are shown. The part containing helix more A second important group of DNA -binding motifs adds one or more zinc atoms as structural components. Although all such zinc-coordinated DNA-binding motifs are called zinc fingers , this description refers only to their appearance in schematic drawings dating from their initial discovery Figure A. Subsequent structural studies have shown that they fall into several distinct structural groups, two of which are considered here. The first type was initially discovered in the protein that activates the transcription of a eucaryotic ribosomal RNA gene. In this way, a strong and specific DNA-protein interaction is built up through a repeating basic structural unit Figure A particular advantage of this motif is that the strength and specificity of the DNA-protein interaction can be adjusted during evolution by changes in the number of zinc finger repeats. By contrast, it is difficult to imagine how any of the other DNA-binding motifs discussed in this chapter could be formed into repeating chains. Figure One type of zinc finger protein. This protein belongs to the Cys-Cys-His-His family of zinc finger proteins, named after the amino acids that grasp the zinc. A Schematic drawing of the amino acid sequence of a zinc finger from a frog protein of this more Figure DNA binding by a zinc finger protein. A The structure of a fragment of a mouse gene regulatory protein bound to a specific DNA site. Another type of zinc finger is found in the large family of intracellular receptor proteins discussed in detail in Chapter Although the two types of zinc finger structures discussed in this section are structurally distinct, they share two important features: Figure A dimer of the zinc finger domain of the intracellular receptor family bound to its specific DNA sequence. Each zinc finger domain contains two atoms of Zn indicated by the small gray spheres ; one stabilizes the DNA recognition helix shown in brown more One group of gene regulatory proteins, however, has evolved an entirely different and no less ingenious recognition strategy. The bacterial met repressor protein. The bacterial met repressor regulates the genes encoding the enzymes that catalyze methionine synthesis. When this amino acid is abundant, it binds to the repressor, causing a change in the structure of the protein more Usually, the portion of the protein responsible for dimerization is distinct from the portion that is responsible for DNA binding see Figure One motif , however, combines these two functions in an elegant and economical way. The helices are held together by interactions between hydrophobic amino acid side chains often on leucines that extend from one side of each helix. The dimer thus grips the double helix like a clothespin on a clothesline Figure A leucine zipper dimer bound to DNA. However, many gene regulatory proteins, including leucine zipper proteins, can also associate with nonidentical partners to form heterodimers composed of two different subunits. Because heterodimers

typically form from two proteins with distinct DNA-binding specificities, the mixing and matching of gene regulatory proteins to form heterodimers greatly expands the repertoire of DNA-binding specificities that these proteins can display. As illustrated in Figure , three distinct DNA-binding specificities could, in principle, be generated from two types of leucine zipper monomer , while six could be created from three types of monomer, and so on. Figure Heterodimerization of leucine zipper proteins can alter their DNA-binding specificity. Leucine zipper homodimers bind to symmetric DNA sequences, as shown in the left-hand and center drawings. These two proteins recognize different DNA sequences, as indicated more There are, however, limits to this promiscuity: Thus each leucine zipper protein in the cell can form dimers with only a small set of other leucine zipper proteins. Heterodimerization is an example of combinatorial control , in which combinations of different proteins, rather than individual proteins, control a cellular process. Heterodimerization is one of the mechanisms used by eucaryotic cells to control gene expression in this way, and it occurs in a wide variety of different types of gene regulatory proteins Figure As we discuss later, however, the formation of heterodimeric gene regulatory complexes is only one of several combinatorial mechanisms for controlling gene expression. Figure A heterodimer composed of two homeodomain proteins bound to its DNA recognition site. During the evolution of gene regulatory proteins, similar combinatorial principles have produced new DNA -binding specificities by joining two distinct DNA-binding domains into a single polypeptide chain Figure Two DNA-binding domains covalently joined by a flexible polypeptide. The flexibility of the loop allows one helix to fold back and pack against the other. As with leucine zipper proteins, the second HLH protein can be the same creating a homodimer or different creating a heterodimer. Figure A helix-loop-helix dimer bound to DNA. The two monomers are held together in a four-helix bundle: These truncated proteins can form heterodimers with full-length HLH proteins, but the heterodimers are unable to bind DNA tightly because they form only half of the necessary contacts. Thus, in addition to creating active dimers, heterodimerization provides a way to hold specific gene regulatory proteins in check Figure Figure Inhibitory regulation by truncated HLH proteins. On the right, the binding of a full-length HLH protein blue to a more It is reasonable to ask, therefore, whether there is a simple amino acid- base pair recognition code: The answer appears to be no, although certain types of amino acid-base interactions appear much more frequently than others Figure As we saw in Chapter 3, protein surfaces of virtually any shape and chemistry can be made from just 20 different amino acids, and a gene regulatory protein uses different combinations of these to create a surface that is precisely complementary to a particular DNA sequence. We know that the same base pair can thereby be recognized in many ways depending on its context Figure Nevertheless, molecular biologists are beginning to understand protein-DNA recognition well enough that we should soon be able to design proteins that will recognize any desired DNA sequence.

Chapter 4 : Helix-Turn-Helix Motif (Molecular Biology)

In proteins, the helix-turn-helix (HTH) is a major structural motif capable of binding calendrierdelascience.com monomer incorporates two Î± helices, joined by a short strand of amino acids, that bind to the major groove of DNA.

Protein-DNA Interactions Helix-Turn-Helix Motif The helix-turn-helix motif is commonly found in proteins that are involved in the regulation of transcription in prokaryotes regulation of gene expression. Examples include the Cro repressor from a bacteriophage, the E. Helix-turn-helix motif structure The general structure of the helix-turn helix HTH motif can be seen here. It is composed of two a-helices: These two helices are separated by a turn. The HTH motif is part of a protein known as the lac repressor. It is a protein involved in the regulation of lactose metabolism. It is composed of two subunits, A in yellow and B in blue. Each monomer of the lac repressor is a protein composed of two domains. The DNA-binding site is found in the N-terminal domain, and the allosteric activator-binding site is between the N-terminal and the C-terminal subdomains. Symmetry of the lac repressor: The symmetry of the lac repressor dimer allows the protein to bind to the DNA about a symmetric binding site. Can you see the symmetry of the two protein subunits as the movie plays? The lac repressor binds to DNA in a fashion that is very specific: This illustration shows the proximity of the various residues to their partner molecule: The dots show residues that are involved in hydrogen bonding. Leucine Zipper Motif The leucine zipper is composed of two a-helices. Each a-helix has a basic region at the N-terminal end that contains several positively charged residues that interact with the major groove of the DNA. Toward the C-terminal of the a-helices, the dimerization region is found. The hydrophobic region that causes dimerization is shown here. The main driving force behind the dimerization is the presence of leucines shown in yellow at every seventh position in the helix. They interact hydrophobically to form a tight dimer structure. The basic region that interacts with the DNA is shown here. Several arginine and lysine residues are present shown in blue. They are able to interact with the DNA phosphodiester backbone. Protein and DNA interactions: The phosphodiester backbone of the bound DNA strand is negatively charged and able to interact with the basic region of the leucine zipper, which is positively charged. Notice how well the DNA and protein fit together. The general interactions that take place between the protein and DNA are the nonspecific charge interactions between the phosphodiester backbone of the DNA and the basic amino acids of the leucine zipper. This associates the DNA and protein together. The next level of interactions is the specific interactions that take place between the nucleotide bases and the amino acids of the protein. These are the interactions that allow sequence-specific interactions between protein and DNA. Zinc Finger Motif Zinc fingers usually occur tandemly with several occurring in a row in their DNA-recognition proteins. They are found in many transcriptional regulators found in eukaryotes. Zinc fingers are the third structural motif for DNA regulatory proteins. The fold consists of an a-helix followed by a turn and two short segments of b-strands separated by a loop. The a-helix and the first b-strand contain conserved cysteine and histidine residues that coordinate with the zinc metal ion that gives the zinc finger its name. It contains nine zinc fingers, six of which are shown in the crystal structure. The zinc finger motif is used canonically, and the interactions between the DNA and protein are not the same between the different zinc fingers. Can you see the difference in interactions for each of the zinc fingers? Commonalities between all binding motifs: Each protein DNA recognition motif is composed of a recognition region and a stabilization region. Protein-DNA recognition takes place at two levels: In the protein, a-helices make most of the base-specific interactions. In the DNA, base-specific interactions happen in the major groove. For more specific instructions on how to use Chime, visit Chime Help.

DOWNLOAD PDF DNA RECOGNITION IN PROCARYOTES BY HELIX-TURN-HELIX MOTIFS

Chapter 5 : DNA-binding domain - Wikipedia

The helix-turn-helix motif was first identified as a conserved sequence element in the repressors encoded by the lambdoid phages of E. coli and Salmonella typhimurium. Subsequently this element has been found in a large variety of DNA-binding proteins, both in prokaryotes and in eukaryotes, and.

Membrane Proteins Breaking News Fromknecht et al Journal of Bacteriology Is this the first step to a new class of drugs? The motif consists of two alpha helices and a short extended amino acid chain between them. The more carboxyl-terminal helix can fit into the major groove of DNA. This motif is found in hundreds of DNA-binding proteins, including lambda repressor, tryptophan repressor, catabolite activator protein CAP , octamer transcription factor 1 Oct-1 and heat shock factor HSF. The protein typically interacts with DNA as a dimer. The HTH motif is sometimes referred to as the "reading head" or "headpiece". The motif typically involves three helical moieties that interact with DNA: Helix 3 is classified as the recognition helix; Helix 2 is called the stabilization helix; Helix 1 serves as an interface to the remainder of the protein. One of the best characterized such motifs is found in the lambda repressor. The subunit folds into two independent globular domains. The C-terminal domain is required for cooperative binding and is not present in this crystal structure. Our goal today is to try to gain an appreciation for the complementary shapes of the recognition helix and the major groove. If you do not see any windows appearing, please follow the instructions here to insure that your web browser is allowing Java Applets to run. There is another, C-terminal, domain in each subunit of the intact dimer molecule of repressor, which was not included in the crystal structure determination. In the start-up view, the DNA double-helix is angled so that you look down the major grooves in which the repressor mainly binds. There is a nearly-exact twofold symmetry between the two subunits of the lambda repressor dimer and between the two halves of the operator site on the DNA, but for subunit b the N-terminal tail is shown wrapped around the DNA it includes 3 lysines while residues of subunit a were disordered in the crystal. Subunit b binds to the half of the DNA that has the consensus operator sequence, while the other half has a non-consensus sequence with 3 changes. The DNA is nearly standard B-form, but it is bent very slightly around the protein. View2 looks down the double helix from one end, with the repressor sitting on top. Only interacting side chains are shown, on the b subunit. The base pairs are shown in full, but without the base-pair Hbonds and without an explicit connection to the DNA backbone; those that make interactions are color coded: G green, C yellow, A pink, and T blue, while the others are in gray. Gln 44, Ser 45, and Asn 55 of both repressor subunits, and Thr 2 and Lys 4 of subunit b, make specific H-bonds with bases in the major groove. View2 is a close-up of the Gln 44 interaction, showing the H-bond network to Gln 33 and a phosphate O that helps determine the nature and orientation of hydrogen bonds to Adenine 4 on strand 2 of the DNA. View3 shows the double side-chain interaction of Asn 55 and Lys 4 with G 14 of strand 1, and also the H-bond between Thr 2 and G View4 looks deep into the interface, to show how the methyl groups of Thymidines 5 and 15 green atom balls fit snugly in between hydrophobic side chains and up against the helix backbone at Gly 46 and Gly View5 looks down the axis of helix 1 of the binding motif from its N-terminal end, in a region that is typical of the types of non-specific DNA-binding interactions made with the sugar-phosphate backbone. The N-terminus of the alpha helix interacts both by a specific H-bond to one of the free NH groups in the first turn, and also by means of the helix dipole, which is appropriately positive at the N-terminus for interacting with the negatively-charged phosphates. That same phosphate group also has a salt link to a charged Lys side chain and an H-bond to a polar Tyr OH group. Everse, All Rights Reserved.

Chapter 6 : Helix-turn-helix - Wikipedia

The helix-turn-helix motif is the common DNA recognition motif in prokaryotes (Voet&Voet, Fig. b). The motif resembles that of an EF hand described in calmodulin. The F-helix is the recognition helix and the side chains give the specificity of

binding.

Chapter 7 : DNA binding proteins: nucleosomes and transcription factors

This result suggests that the sigma 54 helix-turn-helix is involved in recognition of the region of sigma dependent promoters. Full text Get a printable copy (PDF file) of the complete article (M), or click on a page image below to browse page by page.

Chapter 8 : DNA-Binding Motifs in Gene Regulatory Proteins - Molecular Biology of the Cell - NCBI Booksh

DNA recognition motif is combined with a dimerization motif. Two helices are held together by hydrophobic amino acid side chains (e.g. leucine). It forms a Y-shaped structure that allows contact with the major groove of DNA.

Chapter 9 : Helix-turn-helix | Revolvy

The HTH is a short motif made up of an alpha-helix, a connecting turn, and a second helix, which specifically interacts with the DNA and is known as the recognition helix.