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Dna sequence from amino acid sequence

What are the mrna and amino acid sequence for the protein made from the following dna sequence. How to determine dna sequence from amino acid sequence. Predict amino acid sequence from dna sequence. Can we predict the exact dna sequence from an amino acid sequence. Is it possible to determine the dna sequence from the amino acid sequence leu pro arg. Which amino acid sequence can be coded from the dna sequence cag tag cga. Determine the amino acid sequence of a protein from the nucleotide sequence of its dna. Which amino acid sequence can be coded from the dna sequence gct ggg cta.

20 amino acids, their database database codes (SLC), and their corresponding DNA tags SLC DNA Codões isooleucine it, ATC, ATA, CTC, CTA, CTG, TTG, TTG Valine v GTT , gtc, gtt, gtg phenylalanine phenylalanine phenylalanine, ttc methionine m ATG cysteine IC tgt, tgc alanine, gcc, ggt, ggt ic ggt, ggc, ggg, ggg, proline ã, ¬ pc ccc, CCC, CCA, act, ACC , ACA, ACG SERINE, TCC, TCA, TCG, AGT, AGC TirosineÃ ¢ â, Tat, TAC TRYTOPHANÃ © â € ¬ W tgg glutamine Cong and Gaa, Gag The Aging Aging Aspath, AAA, AAG Arginine, CGC, CGA, CGA, CGA A Aga, Agg Stop Codons Stop Taa, TGA in this Table, the twenties amino acids found in proteins are listed, along with the unique letter code used to represent these amino acids in protein databases. DNA tags representing each amino acid are also listed. All 64 Possible combinations of 3 letters of DNA T, C, A and G coding units are used to code one of these amino acids or as one of the three stops that signals the end of a sequence. While DNA can be unequivocally decoded, it is not possible to predict a DNA sequence of your protein sequence. As most amino acids have several types, several possible DNA sequences can represent the same protein sequence. The DNA (deoxyribonucleic) is the genotamic material in the cells that contains the genetic information used in the development and functioning of all known living organisms. DNA, along with RNA and proteins, is one of the three main macromoles that are essential for life. Most DNA is located in the Normal, although a small amount can be found in mitocÃ'ndrias (mitochondrial DNA). Inside the eukaryotic cell core, the DNA is organized in structures called chromosomes. The complete set of chromosomes in a cell compose your genome; The human genome has approximately 3 billion of DNA base pairs organized in 46 chromosomes. The information carried by DNA are maintained in the sequence of DNA pieces called genes. DNA consists of two long polymers of simple nucleotide nucleotes, with backbones made of actions and phosphate groups united by tutulos of is ster. These two wires run in opposite directions and are, therefore, anti-parallel. Attached to every suit is one of four types of molemats called nucleobases (bases). It is the sequence of these four bases along the backbone encoding information. The sequence of these bases comprises the genetic code, which subsequently specifies the sequence of amino acids within proteins. The ends of the DNA wires are called 5 â € â € (Five Prime) and 3 ends (three first). The end of 5 ends has a terminal phosphate group and the terminal 3 terminal of a terminal hydroxyl group. One of the main structural differences between DNA and RNA is the Açúcar, with 2-deoxyiribosis in DNA replaced by RNA ribose. The structure of the DNA bases is classified in two types: the purines, the aege the pyrimidines, the six-membered c, T and U. uracil (U), takes the site of RNA and differ from leit of a methyl group in his ring. Uracil is not normally found in DNA, occurring only as a chyte disaggregation product. In the double DNA, each base type in a slope usually interacts with only one type of base in the other aspect. This is the complementary pairing. Therefore, the purines form bonds of hydrogen to pyrimidins, with a connection only to T, and C, only G. 1.2 The central dogma the central dogma of the molecular biology is Ã ¢ € Å "DNA does the RNA makes protein. This general rule emphasizes the order of events of the transcription through translation and provides the basis for much of the genetic code survey in the double but Lice 1950s. Dogma It is often expressed as the following: â € ™ Â â € œ DNA makes RNA, RNA makes proteins, proteins make us ... ... It is never translated back to RNA or DNA. In addition, the DNA is not directly translated to protein. The central dogma of molecular biology also see: ã, the center dogmaan, (external connection). 1.3 DNA Division Mobile replication is essential for the multiplication of the cells and organisms to grow. As the final step the central dogma, the replication of the DNA should occur in order to convey faithful genetically material to the progeny of any cell or body. When a cell is divided, you should correctly replicate the DNA on your genome so that the two daughters ceases have the same genetically as your parent. The DNA double strand structure provides a simple mechanism for DNA replication. The two chains are separated and then an enzyme DNA polymerase called recreates complementary DNA sequence each stranda s. This enzyme causes the complementary chain to find the correct base by pairing complementary bases. As DNA polymersies can only extend a DNA chain at a 5 Â² to 3a Â² direction, different mechanisms are used. In this way, the base on the ancient chain said that base will appear in the new chain and the sky ends with a perfect copy of your DNA. This process typically occurs during phase S of the cell cycle. 1.4 DNA transcription for RNA The process by which DNA reaches its life and function control through cellular protein synthesis is the expression of the Calledan gene. A gene is a DNA sequence that contains genetic information for a functional protein. Proteins are essential for modulating and maintenance of cellular activities. The formation of new protein molems is made of amino acid construct blocks based on encrypted DNA / RNA information. The amino acid sequence of each protein determines its conformation and properties (for example, the ability to interact with other molems, enzymatic activity, etc.). Directed protein Sunthese follows two main steps: gene transcription and transcription transcript. The transcription is the process by which the genetic information stored in the DNA is used to produce a complementary RNA aspect. In more detail, the sequence of the DNA base is first copied in a RNA molemplate, called RNA of the Pressenger, by RNA messenger polymerase (MRNA). Pressenger RNA has an idless base sequence to the DNA encoding chain. Genes consist of sequences encoding MRNA (exons) that are interrupted by sequences not of variable length encoding, introne called. Introns are removed and exons gathered before the translation started in a process called Splicing of MRNA. Messenger RNA splicing has proven to be an important mechanism to significantly increase the versatility and diversity of the expression of a single gene. It is real in the native in eukaryotes and cytoplasm in bacterial and archaea and takes to the formation of mature mrna. Various different MRNA and protein products may arise from a single gene by selective inclusion or exclusion of individual mature products of MRNA. This phenomenon is called alternative Splicing of MRNA. Allow a single gene to encode several MRNA and protein products with related but different structures and functions1. Once the introns are excised - MRNA's final finish molene, this is then exported to the cytoplasma through nuclear pores, where it binds to protein complexes -Rna called Ribosomes2. Ribosomes contain two subunits: the subunit of the 1960s contain a molemple of single ribosomic RNA, large (28), with several proteins, while the RNA component of the 60's subunit is a molen Minor RNA Cula (18) (18). DNA transcription 1.5 EPIGENATE ALSEMENT Each Sumatic Lula in the Human Body contains the same genome, activation and genes silencing specifically of cellular type. In addition, a calamarium should silence the expression of specific genes for other types of cells to ensure genuine stability. This type of repression must be maintained throughout the life of each cryula in normal development. Epigenic epigenic modifications They are defined as hereditary, but reversible changes that influence the expression of certain genes, but without change in primary DNA sequence are ideal to regulate these events. The best epigenial modification of the human being is the methylation of the DNA, however, it becomes increasingly recognized that the methylation of the DNA does not work alone, but Yes occurs in the context of other epigenic modifications, such as histone modifications. DNA methylation: DNA methylation consists of the addiction of a methyl group to cytosine carbon 5 within the CPG of dinucleotides. DNA regions in the human genome, ranging from 0.5 to 5 kb, which are rich in CG are called CPG islands and are usually found in the genes promoters. Approximately half of all the gene promoters have CPG islands that when methylated lead to transcriptional silencing. The DNA methylation of nine is caused by DNA methyltransferases (DNMT) 3A and 3B, while the maintenance of the methylation of DNA by DNMT1. The aberrant patterns of the DNA methylation were described in various human malignancies. In particular, global hupomethylation has been implicated in the initial stages of carcinogen, while the hypermetylation of tumor suppressor genes was involved in the progression of the Cávente3. DNA hypomethylatia agents are used for the treatment of certain hematolic malignancies. Histon Modifications: The histones are proteins around which DNA winds to form nucleosomes. The nucleosome is the basic DNA packaging unit within the neat and consists of 147 genotian dna base pairs involved twice around a highly preserved histone octamer consisting of 2 copies each of the central histones H2A , H2B, H3 and H4. Histon tails may suffer many chemical modifications, such as acetylation, methylation, phosphorylation, ubiquitylation and sumoilation. It is believed that the combinations of these modifications constitute a codigo, called the "code" of the Histon. "Histon's modifications act except for the condemnation of chromatin and transcriptional repression in vain Other biological processes, including activity of the gene and DNA repair. Epigenic modifications 2. RNA RNA, is another essential macromolymor for all known life forms. As DNA, RNA is compound of nucleotides. Once you think to play papers accessories, the RNAs are now understood among the main regulatory players of a Cello, where they catalyze biological reactions, control and modulate expression GENNY, detect and communicate responses to cellular signals, etc. The chemical structure of RNA is very similar to that of DNA: Each nucleotide consists of a nucleobase a rival and a phosphate group. There are two differences that distinguish The RNA DNA: (a) the RNA contained ribose deçar, while the D In contention of slightly different acoxyiribosis (one type of ribose that does not have an oxygen spot), and (b) the RNA has uracil nucleobase as the DNA contained timina. Contrary to DNA, most RNA molems is stranded and can adopt very complex three-dimensional structures. Families and DInities and RNA The universe of protein coding and protein encoding (NCRNAS) is very diversified vis-Âƒ Bioganis, composition and function , and has been expanding rapidly 5 - 9. Among the NCRNAs, microns (mirnes) represent the most studied class at the date and demonstrate regular expression of their genetic protein coding goals in a way Sequence dependent 10 - 12. 2.1 monocyster versus RNA polycystem An RNA molemplate is monocisterane when it captures the genetically information for a single molecular transcriptional product, e.g. A single precursor of Mirna or a primary mRNA. Most eukaryotic mRNAs are in fact monocystem. On the other hand, RRNAs and some miRNAs are known to be polygres. In the case of mrnas The primary transcription comprises several mrnas back to back, each of which will eventually be translated into a sequence of amino acids (peptide polypeptide). Such polypeptides usually have a Function (often the subunits that compose a complete complex protein) and their coding sequences are grouped in a single primary transcription, which, by their Time, allows you to share a common promoter and be set together. 2.2 RNAs of protein coding / gene expression One of the best known and better classes of RNAs are Messenger RNAs (MRNAS). MRNAS carry the genetic information that directs the synthesis of proteins by ribosomes. All cellular organisms use mrnas. The process of proteins samples makes use of two more classes of RNAs, transfer RNAs (TRNAs) and ribosome RNAs (RRNAs). The role of the trnas is the delivery of amino acids to the ribosome where the rarnas connect together to form proteins. MRNAS: A fully processed mRNA usually comprises exons multiple microwapses that were mounted on a single chain after splicing of the spring primary transcription and the removal of intervening introns. The MRNA molemplate includes a cap, the call region of 5 "not translated (UTR), the coding region, 3Ã ¢ 'TR and a poly tail (A) Variable. 5 ~ â € â € â € â € â € â € "The cap is a modified guanino nucleotide added to the Ã â € œ¬ Å" Â € â € â € ~ â € â € â € â € â € â € â € â € â € ~ â € â € â € £¬) MRNA using a connection of a 5-year triphosphate. This modification is fundamental for adequate recognition and attachment of the RIBOSOMA, as well as protection of exonucleases of 5 regions not translated: Regions not translated (UTRS) are nucleotous stretches which flanked the coding region and are not translated into amino acids. There are two UTRS: the "Prime Region has not translated" or 5Â ¢ 'tr, and the "Prime Region has not translated" or 3-UTR. These regions are part of the primary transcript and remain after the Exon Splicing in the MRNA. As such UTRs are exonite regions. Various functional papers were attributed to intranslaced regions, including the stability of MRNA, MRNA location and translational efficiency. The capacity and nature of the functions performed by a UTR depends on the actual use of the UTR and usually differ from an MRNA to the next. The Translation Efficiency Control of UTRS has been shown to cover the entire spectrum, from improvement to complete inhibition of the translation. RNA connection proteins that bind to 5 or 3 Âµl can influence translation by modulating the ability of the ribosome to bind to MRNA. In addition, the miRNAs linking to the 3rd are also able to affect the translation efficiency or the stability of MRNA. Encoding regions: a subset of the nucleotide sequence that is covered by the exons of the transcription is used to guide the translation in the corresponding amino acid sequence and referred to as the regions encoding. The length of a coding region is always a threethlinth of three, and a direct consequence of the fact that each amino acid requires three nucleic acids (the ~ CodonÃ ¢ CodonÃ ¢ â €) For your definition. As 4 = 64 nucleotide triggers, but only 20 amino acids, it follows that an amino acid data can be encoded by more than one trigÃO. The correspondence between a triple and an amino acid is given by the table of CÃ³on that also defines the "genetic code". The tables of the organisms are widely identical, but small variations were discovered over the last 30 years. . Tags are "â € €" and translated into peptide polymers by ribosome. The coding regions begin with the beginning of the beginning and end with a stopper. In general, the beginning of the beginning is a triple of August and the stop ditch is one of the UAA, UAG or UGA. Poly Tail (a): The variable length 3 'poly (a) tail is a long sequence of adenine nucleotides (many hundreds) added to the 3' end -MRNA end. This tail promotes the export of the Normal, Translation and Stability of the MRNA13,14. The structure of an MRNA 3. Interference of RNA interference RNA is a process that moderates the gene expression Sequence-dependent way. The RNAI path is found in all higher eukaryotes and was recently found on the budding yeast as well. Also. They also demonstrated to be aware of RNAI in which they use the RNAI path of natural host for their benefit. The RNAI is started by Dger, a specific dual-rna RNA endonuclease of the RNase III Protein Family. Dger clinched double-stranded RNA (DSRNA) in short fragments of ~ 21 nucleotides, with a salience of two nucleotides at its end 3 Â Â °², as well as a 5 Â Â Â ° ° and a hydroxyl group. The RNAI path can be engaged by two types of small rns non-regulatory encoders: a) small interfering (SIRNAS) RNAs, which are typically exogenous, and b) microNas (miRNAs), which are endogens. SIRNAs are dual-stranded ncRNAs that are mainly delivered to calama experimentally by various multi-transfection, although they have been described in order to be produced. MiRNAs are another kind of small ncRNAs that are transcribed from the DNA of the organism. After the processing of primary and miRNAS SIRNAS by DGER, usually one of the two wires is loaded in the RNA (RISC)-induced silencing complex, a RNA and protein complex that includes the Argonaut protein, while the other aspect is discarded. Loaded SIRNAS and Mirni Guide Risc Guide for Specific MRNAs (targets). SIRNA / MIRNA sequence determines the identity of the target. The heteroduplex resulting from SIRNA / MIRENA and its target MRNA is characterized by the base pairing that generally covers large part of the length of SIRNA / MIREMA. SIRNAS are typically designed to be perfectly complementary to their goals. On the other hand, the miRNAs do not need to be complementary to the MRNA they target. This correspondence inaccurate the mirnms the potential to segment several endogens mrn¡s simultaneously. If induced by a SIRNA or a MIRRINA, the downstream effect is the regulatory down of the directed MRNA, whether by degradation or translational inhibition. The interference of RNA in mammalian mammals SIRNAS are widely used in the laboratory down - regulate the specific proteins whose functions are under study. At the same time, the ability to engage the RNAI path in demand suggests the possibility that the RNAI can be used in the clinic to reduce the production of these proteins that are super expressed in a certain context of disease §The. Analogously, the RNAI can also be used for Ã â € ™ ¬ "Sponge â € œSentias of an excess of amounts of an endogene mirna that, otherwise, regulating a proteification needed. The delivery method continues to be an important consideration for the development of RNAI based therapies, since the active molemplace needs to be delivered efficiently and specifically tissues in order to maximize the impact and Decrease the effects outside the target. See also: RNAI (external link). 4. RNAs of non-protein coding (AKA not-coding RNA or NCRNA) Protein's expression is determined by genizemic information, and its presence Supports the function of cellular life. The parts of the genome of an organism are transcribed in a specific way of ordered tissue and development in RNA transcriptions intended to carry out the possible production of proteins. Recently recently, it was believed that the molems that are important for the function of a calamarium are those described by the â € ¬ Å "central of dogmaÃ £ o of biology, namely messengers and proteins. Things started to change with the discovery of microRnas for more than 20 years in plants16 and animals17,18. Subsequent research efforts have demonstrated that large parts of the genome of an organism will be transcribed at a time or other in RNA, but will not translate into a sequence of amino acids. These RNA transcript were referred to as NCRNAs and there is an increase in valuation that many of them are actually functional and affect the main cellular processes. There are many recognizable classes of Each with distinct functionality. These include: Transfer RNAs (Trnas) 19; Ribosomal RNAs (RNAs) 20; The aforementioned mirns17,18; small nucleolar rns (Snorts) 21,22; Interacting Piwi. Piwi. RNAs of transcription initiation (tiras) 26; Human micro-displacement (warm) 27; RNAs derived from SNO (SDRNAS) 28; intergenic NCRNA (Lynnvas) 29; etc. The total extension of the distinct classes of NCRNAs that are encrypted within the human genome is currently unknown, but it is believed to be numerous. Non-coding short RNAs: at least three classes of small RNAs are encoded in our genome, based on their biogen mechanism and the type of extra protein that they are associated with mirnes, endogen siras and pirnas. It should be noted, however, that the recent discoveries of numerous small non-canynic rns have a little blurred the boundaries between classes. MicroRNAs (Mirnes): MicroNas (Mirnes) comprise a large family of natural, endogens, endogens and long nucleotide rnas. Mirnes work as the main transcriptional regulators of the constituency of the basic expression by the base pairing with their target mrnas. Originally believed to make its impact exclusively through the 320 target mrnas, since they have demonstrated extensive targets of the coding region as well as 12.31. More than a thousand miRNAs are currently known by the human genome, and each of them has the ability to regulate the expression of possibly thousands of protein coding genes32. In mammals, miRNAs are predicted to control more than 90% of all protein coding genes32. Mirna Bioganesis: ã, micronas (mirnes) are explicitly transcribed by RNA polymerase II or generated from the appropriately long introns of gene protein encoders as a subproduct of splicing. Cannium path on the Cannium Path, the transcription of the primary Mirna Precursor (Pri-Mirna) is performed by RNA Polymerase II. Pri-Mirna is processed in a precursor Mirna (Pre-Mirna) by the â € ™ Â ¢ € € A RNA binding protein. Pronkey -mirnas are Generaly 60-70-nucleotides, have a suspicion of two nucleotides in the end 3 and a group of 3 and 5 phosphate and bends in a characteristic structure similar to Hairpin. Exportina-5 recognizes the characteristic of two 3-nucleotide nucleotides, characteristic of RNase III mediated cleavage, and channels the nuclear pore in the cytoplasm, where it is best processed by Dger, another endonuclease. Dicer pairs with TRBP and pact, both double-RNA RNA binding proteins and clinched -mirna to form a double-stranded 22-nucleotide transitory RNA, again with two nucleotide saliencies in 3 '' End. One of the two wires, typically the one with a relatively smaller stability of base pairing at 5 ends (the thermodynamic asymmetry rule - is referred to as â € ™ ¢ "Guide ¢ â € ™1 and origin For the Ã ¢ â, ¬ "Mature Mirna who associates with the Argonaute protein (ÃƒÂª) to form the RISCS node associated with Mirna (Mirisc) or simply RISC. The second aspect, referred to as Ã â € ™ ¢ "Passenger Ã â €" is typically degraded. However, there were well-documented examples of passenger threads that destroy mature products known as MiRNA * , which are also involved in regulatory activities. The mine helps direct the RISC to targets in a form-dependent manner, mediating the repression of the target expression. Alternative paths (not canna) DROSHA Independent Paths: As mentioned above, most MIRNAs give rise to their own transcription units or derive from the exhets or introns of other genes33 And they require both DROSA and DGer for the cleavage in their maturation. It was recently shown however, first in Draoshophila33 and later in mammals34, that short hair introns, called Mirtrons can be alternative sources of mirnes. Although there are several different differences between mamstrons and invertebrates, both are of Drosha. The mirtrons are short introns with the Pinculus Potential that can be sold and debranched in Imita -mirna and then enter the cananic path. Nuclear, nuclear export, So can be cleaved by Dger and embedded in RISC34. Independent paths of the Dicer: Ã ¢ â € ¢ Independent bioganis of DGer only has been described to MIR-45134. This mirna is processed by Drosha, but yours does not require Dicer. Instead, your -mirna, once charged to behind, is cleaved by the catalactic center to generate an intermediary end of 3, which is more trimmed. It is important to emphasize that the Cataluctical Function of MIR-451 was shown in homozygous automuters that were found to have loss of MIR-451 and died after birth with anemia34. Mirna Biogannesis Mirna: ã, for mirns to pair with target mrnas, a region of Mirna sequence near its final of 5 'needs to be involved in base pairing. The region in question covers nucleotide positions 2 to 7 inclusive and is known as â € ¢ â € â € ¢ Not all nucleotides from the seed region need to be paired for heteroduplex having a functional effect18,35 Âµg "37. The base pairing in the seed region may comprise Watson-Crick's connection , although it is recently needed31, nor enough37.in, whether many years ago that Mirna's connection sites are exclusively in the 3 Â Â Â² of mrnas. However, it was recently shown that the miRNAs of animals may be smoothed the mRNA coding regions equally and extensively31. In the plants, the Mirna target is predominantly through targets of the coding region . The ways in which the miRNAs cause the regulation of their target mrnas was intensely debated. Possible mechanisms include: traditional inhibition38; Removal of the poly tail (a) of mrnas (deenylation 39.40; interruption of captiles of chapter tails 41,42; and, mRNA degradation by Exonucleases43,44, although highly targets Omplementary may be endonucleolytically cleaved45. Other types of mines regulatory function were also described and include translational activation46, heterochromatin 47 formation and DNA methylation 48. Mirna Nomeclature: Each mirna is identified by a name in a single unique. The standard name system uses abbreviated prefixes of three letters to designate the species (for example, HSA - Homo sapiens, which is generally ignored in the literature when the body is implicit), followed by tag of three letters Mir or Mir, followed by a number. The number is allocated by the Mirbase registry. The ripe sequences are designated using the tag Ã â € ‡ â € â € â € "¢ (r), while the precursor capaceles use the tag â € ¢ ¬ Å "Mirarâ €" â "¢" Orthodies in organisms differ only in their name of Espano (eg, HSA-MIRA-101 in humans vs. mamu-mir-101 in mice). Mirnings almost identical that differ in only one or two positions are distinguished by suffixes labeled (for example, MIR-10A and MIR-10B). Paralyzes, this is, the precursors have several cases, i.e. the distinct loci, on the same genome are indicated by numbered suffixes (eg, MIRA-281-1 and MIRA-281-2); Such precursors give rise to idless mature mirnes, but not necessarily with the same cinema. Ultraconservised genes or UCGS: UCGs are NCRNAs that are transcribed from ultra-regions (UCRS) 8,49. The UCRs are genuine segments that have identified 100% preserved between orthylogenic regions in human, mouse and mouse. Of these, 481 are transcribed (T-UCRS) of integennial sequences (39%), introns (43%) while the remainder is exogenous or overlapping EXON50,51. Small Nucleolar RNAs (Snorts): Nucleolar Small RNAs (Snorts) are a highly preserved RNA-evolutionary class and were considered in the most featured NC-RNAS22 classes. Size of intermediate size of 60-300 nucleotides in length and are predominantly found in node52. Two main classes of Snorts were identified that have distinctive and evolving elements of preserved sequence. A group contained the C / D motif of the box, while the In the other group load the H / ACA53 elements. SNORNAS are components of small nucleolar nucleulal ribblower and are involved in the transcriptional modification of RRNAs and some Splicicesomal RNASS52,54,55. In particular, most of the functions of SNORNAS C / D and H / ACA in 2 -O-methylation and pseudoridylation, respectively, of several RNA classes. These modifications are important for the production of efficient ribosomes56. Recently, many â € € "orphanÂ Â Â Â Â Â Â € ‡ € Different cellular processes of RNA modification. Piwi-interacting (pirnas): RNAs of Interagir Piwi (Pirnas) are 25 - 30 nucleotides in length and were found in most methazoos. They are independent of Dger and bind to particular Argonaute proteins called piwi proteins24. These complexes of RNA protein are involved in the silencing of the epigenic and transcriptional gene of transposable and other repetitive elements58,59. Pirs also recently linked to regulation Of the Impressed-DNA methylation60. RNAs of transcription initiation (TIRNAS): transcription initiation RNAs (tiras) are derived from sequences in the same Chain that transcription (TSS) innence sites and are preferably associated with promot Ores rich in GC. They were found to have a modal 18 nucleotide décimo that maps within -60 and +120 TSS nucleotes. They are associated with transcript and highly expressed sites of Binding26 of RNA polymerase II. Human (warm) micro-displacement: RNAs (warm) of microra-offset are generated from sequences immediately adjacent to mature Mir and Mir * loci. They were found in Tunicate Ciona intestinalis, but also in human precursors of microna, although in low levels27.61. The high level of conservation and the example of MIRA-219 with warmned warmth among humans and the Cua suggest that they may have a functional role27.61. Derivatives (SDRANAS): Derivative RNAs (SDRNAS) comprise a new class of small RNAs in Eykariarians. Those derived from H / Aca Snords are predominantly 20 - 24 long nucleotides and originate from the end of 3, where those derivatives of SNORNAS C / D are 17 - 19 NT length or> 27 NT in length and predominantly originated from the end of 5. 28 through a comparison of small human RNA sequencing data sets, was shown that SDRNA accumulation patterns c / d health It preserved in several types of cells, although the proportion of the abundance of different sdrnas of a given Snorna Varied62. Long-coding rns: Long non-coding RNAs are a heterogeneous group of non-coding transcriptions that are longer than 200 nucleotides (a condition / Arbitrarily arbitrarily limit that ignores the possibility of NCRNAs with lengths between 40 and 200) that are involved in several processes. A large number of such RNAs was identified and constitutes most of the transcriptome not mammal encoder. Such RNAs were identified in protein-coding locos and also within the intergenic stretches. Numerous protein coding loci is originating the non-protein RNA, with notable examples â € â €

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