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What are histones what are their functions

What is protein histone? Histones are a family of basic proteins that are associated with DNA in the nucleus and help condense into chromatin, they are alkaline (basic pH) proteins, and allow their positive charges to be associated with DNA. They are within the nucleus of eukaryoclear cells. DNA and histones are packed together to form chromosomes in a nuclear, nucleotic form called chromatin. H1 (or H5), H2A, H2B, H3 and H4, core histones are H2A, H2B, H3, and H4, and linker histones are H1 and H5. H1 and the homogeneous protein H5 are involved in the high-difference structure of chromatin. The other four types of histones are associated with DNA to form nuclei. H1 (or H5) has approximately 220 residues. The other types of histones are small, each consisting of 100-150 residues. Histone histone's primary functions are small DNA strands and impact chromatin regulation. Chromatin is a combination of DNA and proteins that make up the contents of the cell nucleus. Without histones, the unused DNA on the chromosome would be very long. For example, each human cell has about 1.8 meters of DNA, but a wound on histone causes a chromosome of about 120 micrometers when replicated and condensed during mitosis. Dna also plays an important role in regulating chromatin and gene expression because it envelops histones. Histone modification is a shared post-translational strain (PTM) for histone proteins, including methylation, phosphoxidation, acetylation, ubiquitylation, and SUMOylation. Methylation indicates the addition or replacement of the methyl group to the substrate of the atoms (or groups) by the methyl group. Phosphoxidation adds phosphate to the molecule. Acetylation describes the reaction to introducing acetyl functional groups into chemical compounds. The addition of ubiquitin to substrate proteins is called ubiquitin or ubiquitous. SUMOylation is a post-translational modification involved in a variety of cellular processes, such as transporting nuclear cell arsalgia, transcription control, cell stone, protein stability, response to stress, and progression through cell cycles. PTM created in histones can affect gene expression by altering the chromatin structure or recruiting histone modifiers. Histone proteins are used to pack DNA that wraps eight histones into chromosomes. Histone modification works in a variety of biological processes, such as transcription activation/inactivation, chromosomal packaging, and DNA damage/repair. Creative Diagnostics provides high-quality histone-related proteins, antibodies, antigens, and Elisa kits. All products have been researched only. These modifications take place through many other warriors Such as HAT, Sirtuin, HDM, HDAC and HMT. They can silence genes that activate or correspond. 슈퍼 패밀리 패밀리 멤버 링키 H1 H1F H1F0, H1FNT, H1FOO, H1FX H1H1 HIST1H1A, HIST1H1B, HIST1H1C, HIST1H1D, HIST1H1E, HIST1H1T 코어 H2A H2AF H2AFB1, H2AFB2, H2AFV, H2AFX, H2AFY, H2AFY2, H2AFY2, H2AFY2HISH2 HIST1H2AC, HIST1H2AG, HIST1H2AI, HIST1H2AAA2 HIST2H2AA3, HIST2H2AC H2B H2BF H2BFM, H2BFS, H2BFWT H2B1 HIST1HISTH12 BA, HIST1H2BB, HIST1H2BC, HIST1H2BD, HIST1H2BG, HIST1H2BH, HIST1H2BN, HIST1H2209, HIST1H2BO H2B2 HIST2H2BE H2B2 HIST2H2BE H3A3 HIST3H3 H3A3 HIST3H3 H4H4 H4H4H4H4, HIST1H4H4H, HIST1H4H4H, HIST1H4I H44H4H, ETC. WILL CONTINUE TO CHECK HUMAN BEINGS. Thank you very much for your cooperation. Histones are a collection of proteins that connect with the DNA of the nucleus and help condense into chromatin. They are alkaline proteins and allow their positive charge to be associated with DNA. They are within the nucleus of eukaryoclear cells. Nucleosomes consist of DNA that envelops eight histone proteins called histone octamers. DNA and histones are all packed together to form nucleosomes, nucleosoids are packs called chromatin, and 2chromatins form chromosomes. Histone Type- Histone Protein is a two-type core histone linker histone core histone core histone - H2A, H3 and H4 linker histone - H1 and H5 Each histone protein was collected to produce a DNA lab 147 base around 1 octamine nucleomicro particles and these core particles. H2A is critical to packaging DNA in chromium martins. H2A package dna molecules will affect chromatin, packaging process gene expression. H2A is correlated with DNA modification. H2A plays an important role in determining the overall structure of chromatin. H2A has been found to regulate gene expression. H2B is also accompanied by the structure of nucleosomes of beads in the present-world structure. H 3 includes the shape form of chromatin in eukaryotes. It provides the functionality of the main legacy domain and has an extended N-terminal tail. H3 is an important protein in the emerging field of epigenetics, and its sequence varyents and variable deformation states are thought to play a role in the dynamic and long-term regulation of genes. H4 is accompanied by the chromatin structure of eukaryotes. H4 includes acetylation and methylation, which can alter the expression of genes located in DNA associated with parent histone octamers. H1 is the main component of the five histone proteins containing chromatin components in eukaryotes. H1 can not make up a nucleosome beads. It sits at the top of the structure, which has DNA that wraps around nucleosomes. It exists in half of the other four This contributes two molecules to each nucleosome bead. H5 histones are individual proteins involved in the packaging of specific areas of DNA. Histone packaging is formed in the core of the nucleosomes 2 dimer H 2A and H2B and tetramer H3 and H4 accompanying the tricycle structure. Histones are very positively charged and have lysine and arginine residues. Histone modification All histone proteins are chemically modified. Chemical modifications of histones are associated with structural changes that occur during replication and transfer. The three most common types of chemical modifications are: acetylation phosphoxylation phosphoxylation:- All core histones are acetylated. The main target for acetylation is lysine 1, the N-terminal tail of histone H3 and H4. Acetyl occurs in two situations: during DNA replication. Acetylation occurs before it is incorporated into histonenucleosomes. Acetyl group is the addition of lysine amino acids to the core molecules of each histone tail. Acetylation is reversible. Acetylation histone enzyme is acetyl transferase (HATs), commonly known as histone acetylas. Two groups of HAT enzymes act on histones in the chromosome and are associated with the control of transcription. Group B is involved in the assembly of nucleosomes and acting on the newly synthesized histones in the sitosol. Acetylation reduces histone affinity for DNA and possible reduces interactions between individual nucleosomes, which leads to the formation of cro martin fibers. The enzyme histone Deacetylases (HDACs) catalyze the removal of acetyl group (i.e. deacetylation). The hexomatatin is usually found in whereas its arylated in yucromatin. Important effects on nucleosome structures: When replicated, acetylation of histones is needed to make it easier to flinch with new cores. In transcription, similar effects may be needed to allow for related changes in structure, even allowing histone cores to be displaced from DNA. Methylation:- Many lysine and arginine amino acids in the N-end of histones undergo methylation. Methylation in lysine or arginine can be one of three forms. Mono, D, arginine. It is catalyzed by methyl transfer. Methylation of other parts of the N terminal of H3 and H4 histones is connected to both suppressed and active chromatin, and depends on the specific amino acids that are modified in the histone tail. For example: - methylation of the solution at the ninth position of H3 is associated with gene-loaded / chromatinin condensation, while the methylation of lysine in position 4 of H3 is associated with transcription activation. Histone's methylation provides a site for the binding of other proteins that result in changes in chromatin structure. Proteins that bind to methylation Contains a domain called a chromo domain. Histone lysine methylation plays an important role in the formation of heomaro chromatin, chromosome X-inactivation, genomic appalization and transcription control. Phosphoxidation:- Histones are phosphineed periodically during the cell cycle and in two situations associated with chromatin remodeling. Histone H1 has been ingring in mitosis and in recent years it has been found that H1 is an extremely good substrate for Cdc2 kinases that control cell division. The enemy of kinases that have inton H3 in 10 Ser has a deadly chromatin structure. Most of the causes of abort structures are likely to fail the man-in-side histone H3. This suggests that H3 phosphoxidation is needed to produce a more expanded chromosomal structure of the colored area. It is important in the cell cycle and is likely to be a single for condensation. The effect of chromatin remodeling seems to be quite the opposite. Of course, phosphation of other histones, or phosphoxidation of other amino acids has the opposite effect on the chromatin structure, adding residues to one histone. References and sources 1% – 1% – 1% – 1% – 4% –

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