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In Silico Study of Post-Translational Modifications of Mammalian Protein Protamine-P1

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Abstract: The protamines are small arginine-rich proteins that are synthesized in the late-stage spermatids of many animals and plants and bind to DNA, condensing the spermatid genome into a genetically inactive state. Vertebrates have from 1 to 15 protamine genes per haploid genome. Both P1 And P2 have been shown to be required for normal sperm function in primates and many rodents. Protein analysis done with the help of software. We show that histone modifications and removal are independent of protamine synthesis. Protamines and transition nuclear proteins are involved in the condensation of sperm chromatin and are expected to affect the shape of the sperm head.

keywords: Insilico analysis, protamine, protein modification

Introduction: The protamines are a diverse family of small arginine-rich proteins that are synthesized in the late-stage spermatids of many animals and plants and bind to DNA, condensing the spermatid genome into a genetically inactive state. Vertebrates have from one to 15 protamine genes per haploid genome, which are clustered together on the same chromosome. Comparison of protamine gene and amino-acid sequences suggests that the family evolved from specialized histones through protamine-like proteins to the true protamines. Structural elements present in all true protamines are a series of arginine-rich DNA-anchoring domains (often containing a mixture of arginine and lysine residues in non-mammalian protamines) and multiple phosphorylation sites. The two protamines found in mammals, P1 and P2, are the most widely studied. P1 packages sperm DNA in all mammals, whereas protamine P2 is present only in the sperm of primates, many rodents and a subset of other placental mammals. P2, but not P1, is synthesized as a precursor that undergoes proteolytic processing after binding to DNA and also binds a zinc atom, the function of which is not known. P1 and P2 are phosphorylated soon after their synthesis, but after binding to DNA most of the phosphate groups are removed and cysteine residues are oxidized, forming disulfide bridges that link the protamine together.

Materials and Methods: To analyses the protein Protamine P1 the amino acid sequence of human Protamine P1 was retrieved from NCBI site and was used for analysis in PepTool 2.0 demo version.

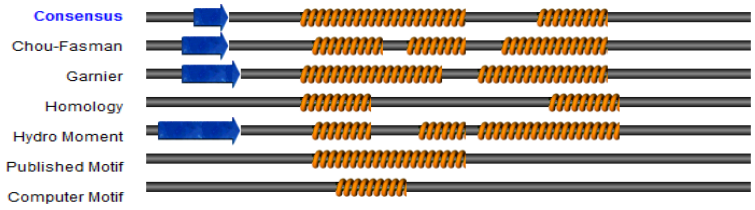
Method For Obtaining Protein Sequences in FASTA Format: -

Google window of internet explorer was opened. Wrote NCBI, pressed enter, NCBI home page was displayed. On home page, wrote protein name, got list of animals in display box. Clicked one by one on names of animals, sequences of protein were displayed. Copied required information of animals. Then clicked on FASTA. Amino acid sequence of a protein in FASTA format was displayed. Copied the sequence and pasted into MS word. Copied as many as larger number of sequences as possible.

Observation And Results:

PROTEIN ANALYSIS: -

Amino Acid Sequence of Protamine P1in Human: Total amino acids- 51



Post Translational Modifications:

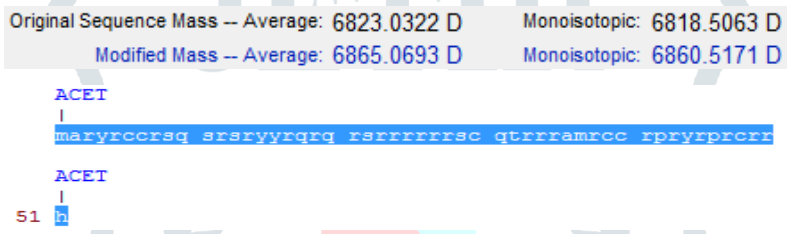


Fig-Acetylation

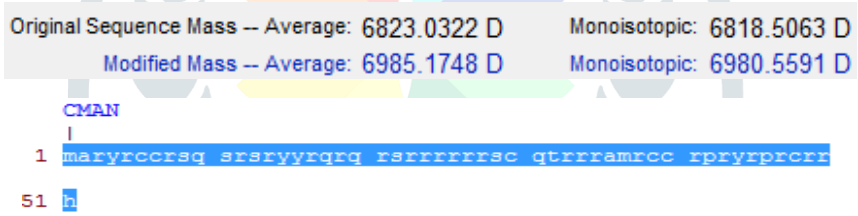


Fig-Mannosylation

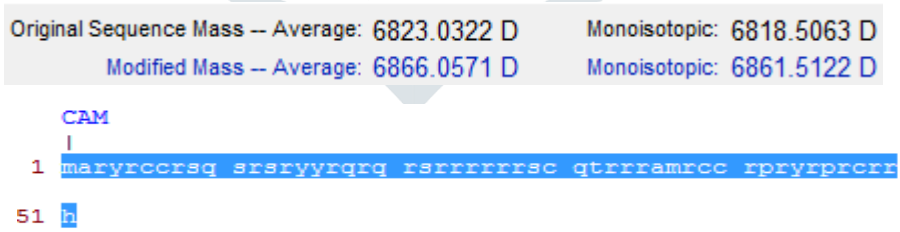


Fig-Carbamoylation

Discussion:

Acetylation: - Acetylation is any chemical reaction that adds an acetyl chemical group is (CH_3CO) called as acetylation. It is occurs generally on lysine residue of protein.

Acetylation is occurs on Methionine at position of 1 and Histidine at position 51.

Mannosylation: - The formation of mannose glycoside, especially one of a protein is called as Mannosylation. Mannosylation occurs on Methionine at position 1.

Carbamoylation:- Transfer of the carbamoyl from a carbamoyl- containing molecule (carbamoyl phosphate) to an acceptor moiety such as amino group. is called as Carbamoylation. Carbamoylation occurs on Methionine at position 1.

Conclusion :

From the results and discussion of present *in silico* protein analysis study of vertebrate Protamine P1 it can be concluded that post translational modification increase the functional Diversity of protein by the covalent addition of functional group on specific amino acid residues.

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