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**IDENTIFICATION OF PROTEOMIC SEQUENCES USING DSP
TECHNIQUES**

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ABSTRACT

For the last several decades, one of the most important areas of biological sequence study has been the quest for hidden periodicities and symbolic patterns. The discovery of physiologically significant motifs like as protein coding regions (exons), CpG islands, and hot-spots relies heavily on periodic components and patterns. A growing number of researchers are using digital signal processing (DSP) to analyse biological sequences. After converting biological sequences to numerical sequences, a variety of DSP algorithms have been developed in order to uncover hidden periodicities and repeating patterns. Some of the most pressing issues in biological sequence analysis are addressed here. This method may be used to analyse RNA, deoxyribonucleic acid, and protein sequences. Signal processing methods are critical to the processing of genomic and proteomic data because of the enormous amount of publically available data. A protein's biological activity is determined by its amino acid sequence. Analyzing a biological function's unique frequency (hot spots) is an essential part of protein sequence analysis. Onco-gen protein sequences and human hemoglobin, HIV, and HIV sequences indicate the usefulness of this technique.

Keywords: Amino Acids, Deoxyribonucleic Acid Sequences, Genomes, Proteomics.