

# MultiProt: A Web based Computational Tool for Protein Parameters

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**Abstract**—The cost of functional genomics by wet lab experiments to predict the biological properties of protein is time consuming and very costly. The protein extraction process is very cumbersome right from protein isolation to purification, 3D crystallography of protein, instability of protein, different bioassay often compromises in terms of predicting accurate function. With availability of genome sequenced data, protein secondary structure prediction and function is no more dependent on traditional methods. Now computational tool can predict secondary, tertiary and quaternary structure with likelihood of post translational modifications. Such predictive methods has accelerated the knowledge discovery of new biological proteins with their functional prediction supplementing proteomic studies. We found one major limitation in use of the available protein data bank (ExPASy ProtParam tool) in extraction of the parameters of a given amino acid sequence. User has to take each sequence manually which is very cumbersome and time consuming for batch of peptides to predict their functions. Script has been written using perl and bioperl to compute all 31 physico-chemical protein parameters. For user friendly and much wider use, a web based application has been using WAMP Server with Apache, PHP and HTML. This tool can be used across all biological kingdom right from microbes to animal, plant fish and insects for throughput retrieval of features of a given amino acid sequence dataset. Predictive biological functions drastically reduces the time and cost with increase in accuracy of function. Thus this tool is of immense use in selecting the protein based on their predicted functions especially before bioassay of proteins.