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Research Article **Published Date:-2017-10-11 00:00:00**

[In silico analysis and characterization of fresh water fish ATPases and homology modelling](#)

ATPases is known to be a crucial in many biological activities of organisms. In this study, physicochemical properties and modeling of ATPases protein of fish was analysed using In silico approach. ATPases a protein selected from fish species, including Gold fish (*Carassius auratus auratus*), Zebra fish (*Hypancistrus zebra*), White fishes (*Coregonus autumnalis*), Grass carp (*Ctenopharyngodon idella*) and Anabas testudineus (Koi) were used in this study. Physicochemical characteristics showed with molecular weight (25045.58-25148.57Da), theoretical isoelectric point (9.30-9.97), extinction coefficient(26470-34950), aliphatic index(147.31-150.35), instability index(32.84-42.67), total number of negatively charged residues and positively charged residues (5/7-6/8), and grand average of hydropathicity (1.014-1.151) were computed. All proteins were classified as transmembrane proteins. In secondary structure prediction, all proteins were composed of random coils as predominant, followed by extended strands, alpha helix and beta turn. Three dimensional structure of protein were predicted and verified as good structures. All model structures were evaluated being accepted and reliable based on structural evaluation and stereo chemical analysis.

Review Article **Published Date:-2017-08-28 00:00:00**

[Microarray Analysis of Fish Genomic Data for enhancing Aquaculture Productivity of India](#)

This review gives a brief introduction to the microarray technology and its experimental design and data analysis and a discussion of recent global progress in research using microarray technology in fish biology and aquaculture. DNA microarrays have been reported to have been used for the analysis of gene expression during various physiological, developmental or cellular processes in fish. During the recent past, investigators have begun to use microarrays on fish to address ecological, evolutionary and environmental questions including the variability of gene expression in natural populations, speciation, ecotype diversity, environmental remediation and host-pathogen interactions. The study suggests that a lot of gene expression studies have been conducted on salmon and zebrafish in Europe and USA. The same may be applied on Indian Major Carps and Catfishes to augment productivity from aquaculture sector.

Short Communication **Published Date:-2017-06-23 00:00:00**

[Function Prediction of Proteins from their Sequences with BAR 3.0](#)

Protein functional annotation requires time and effort, while sequencing technologies are fast and cheap. For this reason, the development of software tools aimed at predicting protein function from sequences can help in protein annotation.

In this paper, we describe how to use our recently implemented Bologna Annotation Resource (BAR) version 3.0, a tool based on over 30 million protein sequences for protein structural and functional annotation. In BAR 3.0, sequences are arranged in a similarity graph and then clustered together when they share at least 40% sequence identity over 90% of sequence alignment, for a total of 1,361,773 clusters.

Protein sequences with known function transfer their annotation to other sequences in the same cluster after statistical validation. Sequences with unknown function and new sequences entering in a cluster inherit its statistically validated annotations.

The method we compare to other techniques in the Critical Assessment of protein Function Annotation algorithms (CAFA). The CAFA experiment tests the performances of different predictors on a dataset that accumulates annotations over time. BAR predictions have been submitted to all the instances of CAFA through the years (BAR Plus in CAFA, BAR++ in CAFA2 and BAR 3.0 in CAFA3). The benchmarking indicates that in the field improvement is still possible and that our BAR scores among the top performing methods.

This work focuses on how the tool can transfer statistically significant features to poorly annotated or new sequences derived from transcriptomics or proteomics experiments.
