Editorial

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Biochemistry & Molecular Biology Journal
ISSN 2471-8084

2021
Vol.7 No.5:24

Editorial Note on Functional Genomics

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Received: May 20, 2021; **Accepted:** May 25, 2021; **Published:** May 30, 2021

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Citation: De Oliveira RJ (2021) Editorial Note on Functional Genomics. Biochem Mol Biol Vol.7 No.5:24

Editorial

Functional genomics is a field of molecular biology which describes gene and protein functions and its interactions. Functional genomics makes use of the major data generated by genomic and transcriptomic projects such as genome sequencing projects and RNA sequencing. Functional genomics focuses on the dynamic aspects such as translation, gene transcription, regulation of gene expression and protein–protein interactions, as opposed to the static aspects of the genomic information such as DNA sequence or structures.

The main aim of functional genomics is to understand the function of genes or proteins, eventually all components of a genome. The term functional genomics is used to refer to the many technical approaches to study an organism's genes and proteins, including the biochemical, cellular, or physiological properties of each and every gene product. Functional genomics also include studies of natural genetic variation over time such as an organism's development as well as functional disruptions such as mutations.

Functional genomics includes function-related aspects of the genome itself such as mutation and polymorphism such as single nucleotide polymorphism analysis and the measurement of molecular activities. Gene function can be investigated by systematically knocking out genes one by one. This is done by either deletion or disruption of function such as by insertional mutagenesis and the resulting organisms are screened for phenotypes that provide clues to the function of the disrupted gene.

CRISPR-Cas9 has been used to delete genes in a multiplexed manner in cell-lines. Quantifying the amount of guide-RNAs for each gene before and after the experiment can point towards essential genes. If a guide-RNA disrupts an essential gene it will lead to the loss of that cell and hence there will be a depletion of that particular guide-RNA after the screen.

In a recent CRISPR-cas9 experiment in mammalian cell-lines around 2000 genes were found to be important in multiple cell-lines. Putative genes can be identified by scanning a genome for regions likely to encode proteins which are based on characteristics such as long open reading frames, transcriptional initiation sequences and polyadenylation sites. A sequence identified as a putative gene should be confirmed by further evidence such as similarity to cDNA or EST sequences from the same organism, similarity of the predicted protein sequence to known proteins, association with promoter sequences or the evidence that mutating the sequence produces an observable phenotype. New computational methods have been developed for understanding the results of a deep mutational scanning experiment.