Journal of Proteomics & Bioinformatics

ISSN: 0974-276X

Editorial

Editorial on Genomics

Susan Williams

Managing Editor, Journal of Proteomics & Bioinformatics, Spain

EDITORIAL

Genomics may be defined as the study of all of a person's genes (the genome), including interactions of those genes with each other and with the person's environment. The main part of genomics is determining the sequence of molecules that make up the genomic deoxyribonucleic acid (DNA) content of an organism. The chemical name for the molecule that carries genetic instructions in all living things called Deoxyribonucleic acid (DNA).

Genome is an organism's complete set of DNA and every single cell in the body contains a complete copy of the approximately 3 billion DNA base pairs, or letters, that make up the human genome.

Specifically genes are transcriptional units, those regions of chromosomes that under appropriate circumstances are capable of producing a ribonucleic acid (RNA) transcript that can be translated into molecules of protein. Proteins make up body structures like organs and tissue. They are of great nutritional value and are directly involved in the chemical processes essential for life.

DNA sequencing is a technique used to determine the sequence of nucleotide bases (As, Ts, Cs, and Gs) in a piece of DNA. The nucleotide sequence tells scientists the kind of genetic information that is carried in a particular DNA segment. DNA sequencing carry the instructions for building an organism, and no understanding of genetic function or evolution could be complete without obtaining this information.

Next-generation sequencing (NGS) is most common type of sequencing used today and describes a number of different modern sequencing technologies. NGS allows researchers to: Rapidly sequence whole genomes, Zoom in to deeply sequence target regions, Analyze epigenetic factors such as genome-wide DNA methylation and DNA-protein interactions, Sequence cancer samples to study rare somatic variants, tumor subclones, and more, Study the human microbiome and discover novel pathogens, Utilize RNA sequencing (RNA-Seq) to discover novel RNA variants and splice sites, or quantify mRNAs for gene expression analysis.

The Human Genome Project was completed in 2003 and was led at the National Institutes of Health (NIH) by the National Human Genome Research Institute. This project produced a very high-quality version of the human genome sequence that is freely available in public databases and generated a resource that could be used for a broad range of biomedical studies.

The major applications of genomics include: the study of genes, or genetics in cases of birth defects, cancer, diabetes, and cardiovascular disease, functional genomics, gene identification by microarray genomic analysis, comparative genomics (study of evolutionary relationships), enabling medical researchers to develop improved diagnostics, more effective therapeutic strategies, evidence-based approaches for demonstrating clinical efficacy, and better decision-making tools for patients and providers.

REFERENCES

1. https://www.genome.gov/about-genomics/fact-sheets/A-Brief-Guide-to-Genomics
2. https://www.genome.gov/genetics-glossary/Deoxyribonucleic-Acid
3. https://www.illumina.com/science/technology/next-generation-sequencing.html
4. https://www.britannica.com/science/genomics

***Corresponding author**: Susan Williams, Managing Editor, Journal of Proteomics & Bioinformatics, Spain, Tel: +44 7480022449; E-mail: proteomics@peerreviewedjournals.com

Received Date: January 05, 2021, **Accepted Date:** January 16, 2021, **Published Date:** January 22, 2021

Citation: Williams S (2021) Genomics. J Proteomics Bioinform 14: 1. doi: 10.35248/0974-276X.1000521