

Difference between genomics and proteomics in whole genome study

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DESCRIPTION

The study of an organism entire gene pool or genetic makeup is known as genomics while proteomics is the investigation of all proteins. DNA sequencing, gene mapping, evolution, gene editing, function, and expression are all involved. It considers each gene that is present in an organism, how they interact, and how they function inside that organism. To analyse the entire genome, high throughput sequencing methods and bioinformatics are required. Epistasis, pleiotropy, and other gene-gene interactions are studied as part of genomics on the other side proteomics aids in comprehending a cell type properties and operations. The whole collection of proteins that are expressed in an organism from its DNA is known as the proteome. A cell or an organism response varies with time, necessity, internal and external environment, stress, etc. Since proteins are the functional byproduct of the genome, proteomics relies on genomic research. Purification, identification, structural analysis, interaction, and functions of proteins are all part of proteomics. This makes use of technologies like mass spectrometry and immunoassay. It offers insight into a biological system. Proteomic examination of cells, organs, and bodily fluids has provided important new understandings into the intricate mechanisms affecting human biology. Proteins serve as intermediary disease phenotypes and shed light on the molecular relationships between clinical outcomes and genetic and non-genetic risk factors. In addition to exposing disease-associated pathways, associations between protein levels and DNA sequence polymorphisms that co-localize with risk alleles for prevalent diseases can also disclose potential therapeutic targets and translational biomarkers. Proteomic data studies on a population- and genome-wide scale, however, are still in their infancy stage. Thanks to spectacular advances in the techniques for identifying proteins separated by two-dimensional electrophoresis and in methods for large-scale analysis of proteome variations, proteomics is becoming an essential methodology in various fields of plant biology. Linking gene expression to cell metabolism on the one hand and to genetic maps on the other, proteomics is a central tool for functional genomics. The study of genomes, or the entire set of genes or genetic material present in a cell or creature, is known as genomics.

The field of molecular biology known as proteomics investigates the collection of proteins that an organism's genome expresses. The study of an organism's genes is known as genomics. Proteomics is a useful addition to genomics and is helpful when researchers wish to test their gene-based ideas. A multicellular organism has one set of genes shared by all cells, but distinct tissues create various sets of proteins that are regulated by gene expression. The proteome is the result of the interaction between environment and the genome, which is referred to as phenotype, whereas the genome is the complete amount of genetic information encoded in the organism and is also known as its genotype. Particularly in eukaryotes, the proteome is greater than the genome as there are more proteins than genes. Alternative gene splicing and post-translational changes like glycosylation and phosphorylation are to main factor behind this. The majority of genes have the necessary instructions to produce the useful molecules known as proteins. (Some genes provide regulatory substances that aid in the cell's protein synthesis.) Within each cell, the process from gene to protein is intricate and tightly regulated. It consists of two primary steps: transcription and translation. Each gene's code can be altered to make two, three, or four distinct proteins. For instance, a large portion of the risk for Alzheimer's disease is caused by three differences in the spelling of one protein. All protein variations, though, are not detrimental. The study of genomes, or the entire set of genes or genetic material present in a cell or creature, is known as genomics. The field of molecular biology known as proteomics investigates the collection of proteins that an organism's genome expresses.

CONCLUSION

The study of an organism's genes is known as genomics. Genomics led to proteomics (*via* transcriptomics) as a logical step. Genome knowledge can be used to study proteomes since genes code for mRNAs, and mRNAs encode proteins. Not all mRNAs are translated into proteins, despite the fact that mRNA analysis is a positive step. It was a logical progression from genomics to proteomics (through transcriptomics). Since genes code for mRNAs and mRNAs encode proteins, knowledge of

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the genome can be utilised to study proteomes. Even though mRNA analysis is a good first step, not all mRNAs get translated into proteins. Since proteins are the functional byproduct of the genome, proteomics relies on genomic research. Purification, identification, structural analysis, interaction, and functions of

proteins are all part of proteomics. This makes use of technologies like mass spectrometry and immunoassay. Genomics can be said as the base need for proteomics and its development.