

Difference Between Proteomics and Transcriptomics

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Key Difference - Proteomics vs Transcriptomics

The omic technology is a current trend, where the different biomolecules of an organism are looked upon as a whole collection with regards to its properties and functions. The omic technology has a wide array of applications. The different omics of a biological sample includes [genomics](#), [proteomics](#), transcriptomics and metabolomics. Proteomics involves the complete study of all [proteins](#) in a living organism. It is defined as the set of all expressed proteins in an organism, its structural and functional properties. The complete set of proteins, therefore form the proteome. Transcriptomics is the complete study of all the messenger [RNA \(mRNA\)](#) molecules present in a living organism. Thus, transcriptomics deals with the [genes](#) that are actively expressed in a living organism. The total set of mRNA in a living organism is referred to as the transcriptome. The **key difference** between Proteomics and Transcriptomics is based on the type of the biomolecule. **In proteomics, the total set of expressed proteins in a living organism is studied, whereas in transcriptomics the total mRNA of a living organism is studied.**

What is Proteomics?

The term proteomics was coined in the year 1995 and was initially defined as the total protein complement in a cell, tissue or an organism. With the advancement in proteomic studies, it was then modified to be considered as an umbrella term in which many study fields were included. Currently, under the topic proteomics, the structure, orientation, functions, its interactions, its modifications, its applications and the importance of proteins are studied. Therefore, much research is conducted in the field of proteomics at present.

The first proteomic studies were done to identify the protein content in *Escherichia coli*. The mapping of the total protein content was done using two dimensional (2D) gels. Upon the success of this, scientists moved on to characterizing the total protein contents in animals such as [guinea pigs](#) and mice. At present, human protein mapping is done using 2D gel [electrophoresis](#).

There are many advantages of studying proteomics, as proteins are the governing molecules of most of the activity due to the catalyst property of proteins. Thus, the study of whole proteins can provide information regarding the health status of an organism. Some applications are;

1. [Genome](#) annotation: By studying the protein content of an organism, the exact genomes responsible for the active protein compound can be determined. In this scenario results from all genomics, Transcriptomics and proteomics are important.
2. Disease identification / Diagnostics: Proteomics is used in the identification of the disease condition, by comparing the healthy and the diseased

3. To carry out protein expression studied during experimentation.
4. Protein modifications and interaction studies: In order to use proteins in *in vitro* conditions or and *in vivo* conditions, to decide the storage conditions of these extracted proteins and to study the behaviour of the protein in *in vitro*, *in vivo* and in – silico methods.

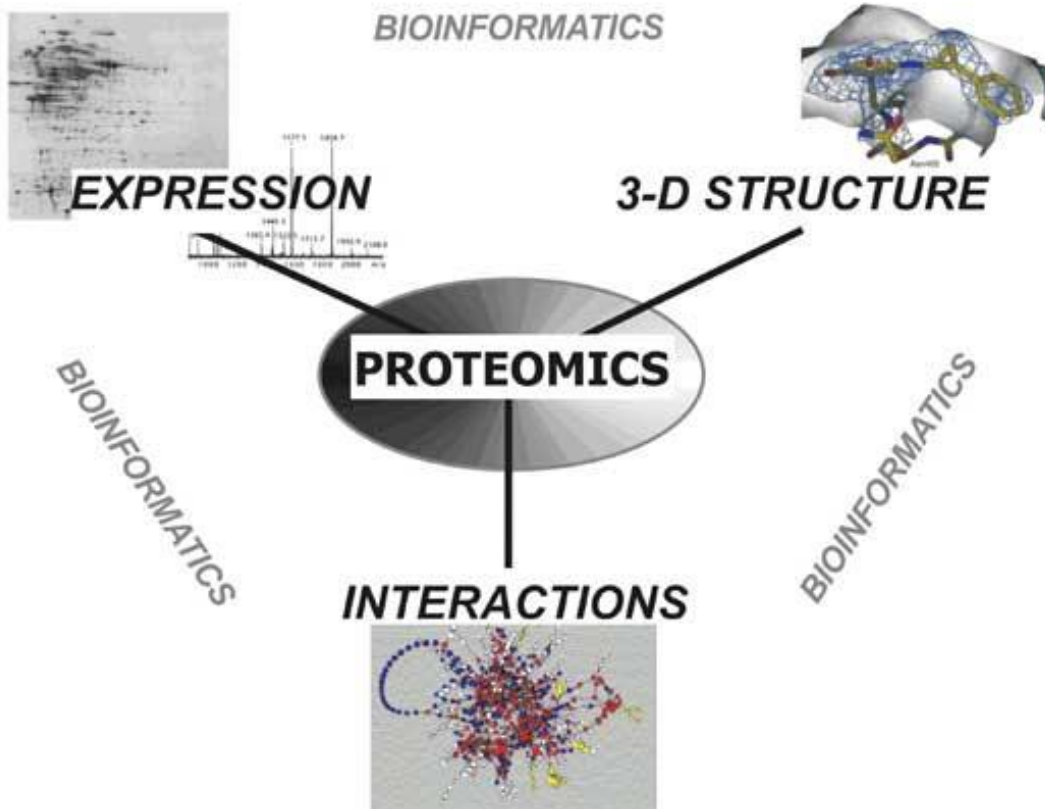


Figure 01: Proteomics

There are different techniques involved in proteomics

1. Extraction of the total protein and separating the proteins using 2D gel electrophoresis. Proteins can also be separated using High-Performance Liquid Chromatography (HPLC).
2. Sequencing of the extracted proteins using methods such as Edmund's sequencing method or Mass spectrometry.
3. Once the sequences are identified, structural and functional properties of the protein content are analyzed using computer-based software and bioinformatics tools.

What is Transcriptomics?

The transcriptome term is coined a recently. The Transcriptomics is the study of the total mRNA content of an organism. The total mRNA is the expressed DNA in a living organism or a cell. The complete collection of mRNA is referred to as a transcriptome.

The steps towards analyzing the transcriptome include,

1. Extraction of RNA, separation of mRNA using column gel chromatography with poly DT beads.
2. The sequencing of the mRNA is done.

Microarray technology is one common way of identifying the transcriptome of an organism. The microarray technique involves a probe plate with the complementary strands of the transcriptome. Upon [hybridization](#), the mRNA present in the organism or cells can be characterized.

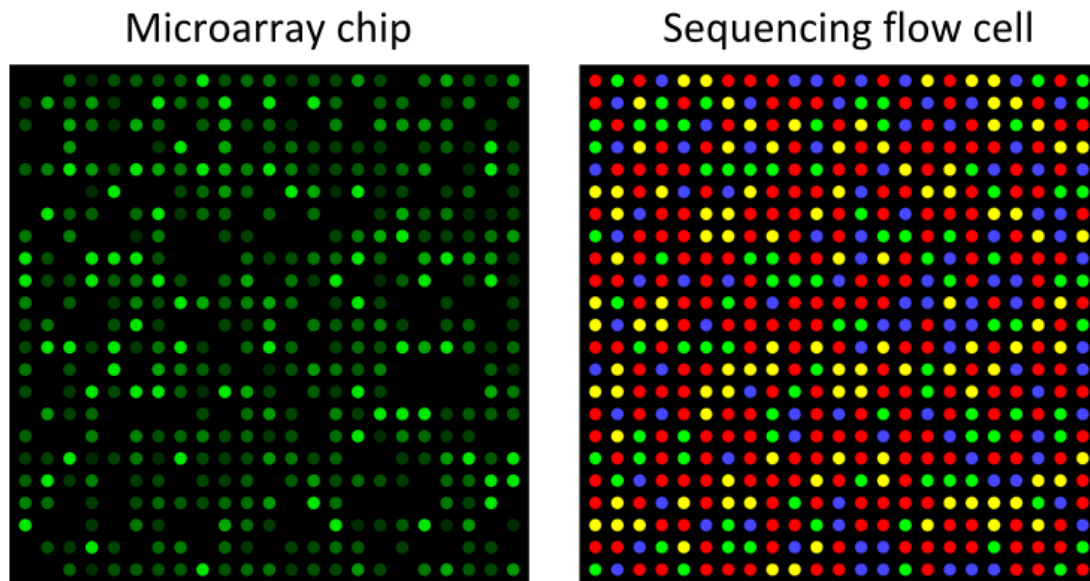


Figure 02: Transcriptomic Techniques

Transcriptomics is now widely used in the medical field. Disease diagnostics and disease profiling are main fields in which Transcriptomics is used. By analyzing a transcriptome of an organism, foreign mRNA can be identified, and if there are any infections, it can be identified. The non – coding RNA can be separated using transcriptomic technologies. And also the expression of genes under different environmental stresses can be monitored.

What are the Similarities Between Proteomics and Transcriptomics?

- Both form a part of the concept of omic technology.
- Both are used in disease diagnostics and disease characterization of an organism.
- Both study areas involved extraction of the biomolecule, separation of the biomolecule and sequencing steps.

What is the Difference Between Proteomics and Transcriptomics?

Proteomics vs Transcriptomics	
Proteomics involves the complete study of all proteins in a living organism.	Transcriptomics is the complete study of all the messenger RNA (mRNA) molecules present in a living organism.
Studied Bio Molecule Type	
Proteins are studied in proteomics.	mRNA are studied in transcriptomics.
Factors Studied	
Structure, function, interactions, modifications and applications of the proteins are studied in proteomics.	Sequence structure, interactions with environment and applications of the mRNA are studied in transcriptomics.

Summary - Proteomics vs Transcriptomics

Omics play an important role in the field of life sciences. Proteomics refers to the study of the proteome which forms the complete collections of proteins in a cell or an organism. Transcriptomics refers to the study of the transcriptome which is the complete set of expressed DNA that is in the form of mRNA. The two study areas, proteomics and transcriptomics, were derived after the introduction of genomics and currently used widely in medical diagnostics and in characterization and screening of organisms. This is the difference between proteomics and transcriptomics.

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