Transcriptomics

- Ectopic expression of GDF15 in cancer-associated fibroblasts enhances melanoma immunosuppression via the GFRAL/RET cascade
- Brain-derived exosomal hemoglobin transfer contributes to neuronal mitochondrial homeostasis under hypoxia
- Transcriptomic analysis reveals novel targets in benign schwannoma using machine learning
- Genetic profiling of synchronous pituitary corticotroph adenomas
- Gasdermin E in glioblastoma -pyroptosis resistance and tumor-promoting functions
- Pro-repair macrophages driven by CGRP rescue white matter integrity following intracerebral hemorrhage
- MitCOM-based prognostic model identifies GLUD1 as a key suppressor of glioblastoma growth and invasion through regulation of mitochondrial structure and metabolism
- Mutations in PSEN1 predispose inflammation in an astrocyte model of familial Alzheimer's disease through disrupted regulated intramembrane proteolysis

Transcriptomics is a branch of molecular biology and genomics that focuses on the study of the transcriptome, which is the complete set of RNA transcripts produced by the cells of an organism at a specific time or under specific conditions. These RNA molecules are typically categorized into two main types: messenger RNA (mRNA), which carries the genetic information from DNA to the ribosomes for protein synthesis, and non-coding RNA, which includes various functional RNA molecules that do not code for proteins but play important roles in gene regulation and other cellular processes.

Transcriptomics involves the analysis of the structure and quantity of RNA transcripts within a cell, tissue, or organism, and it provides insights into gene expression, regulation, and function. Here are some key aspects of transcriptomics:

Techniques: Transcriptomics relies on a variety of experimental techniques for RNA analysis, including:

RNA Sequencing (RNA-Seq): This high-throughput technique is widely used to quantify and profile the entire transcriptome, providing information on gene expression levels, alternative splicing, and novel transcripts.

Microarray Analysis: While less commonly used today, microarrays can still provide valuable information about gene expression patterns.

Northern Blotting: A traditional method used to study specific RNA transcripts.

Applications:

Gene Expression Profiling: Transcriptomics allows researchers to assess which genes are actively transcribed under different conditions, such as in response to environmental stimuli or during various developmental stages.

Functional Annotation: It helps in understanding the functions of genes and identifying pathways and networks in which they are involved.

Disease Research: Transcriptomics is crucial for studying the molecular basis of diseases, including cancer, autoimmune disorders, and neurodegenerative diseases, and for identifying potential

diagnostic or therapeutic targets.

Pharmacogenomics: It plays a role in personalized medicine by understanding how individual genetic variations affect drug responses.

Key Concepts:

Gene Expression: Transcriptomics provides a snapshot of which genes are turned on (expressed) and to what extent. This is essential for understanding cellular processes and responses to various stimuli.

Alternative Splicing: Transcriptomics can reveal how a single gene can produce multiple mRNA variants by alternative splicing, leading to protein diversity.

Non-Coding RNA: Transcriptomics has highlighted the importance of non-coding RNA, including microRNAs, long non-coding RNAs, and small interfering RNAs, which play vital roles in gene regulation.

Data Analysis: Managing and analyzing large transcriptomics datasets requires bioinformatics tools and software to process and interpret the data. This may involve normalization, differential gene expression analysis, pathway analysis, and clustering.

Challenges: Transcriptomics can be challenging due to issues such as data variability, data interpretation, and the need for computational expertise for data analysis.

Transcriptomics is a fundamental tool in molecular biology and genetics, providing valuable information about the dynamic nature of gene expression and how it contributes to various biological processes and diseases. It has become a cornerstone of genomics research, enabling scientists to gain a deeper understanding of the genetic and molecular mechanisms that underlie complex biological systems.

RNA epitranscriptomics.

Spatial transcriptomics