Gene signature

- Predicting podoplanin expression and prognostic significance in high-grade glioma based on TCGA TCIA radiomics
- Interrogation of macrophage-related prognostic signatures reveals a potential immune-mediated therapy strategy by histone deacetylase inhibition in glioma
- Novel drug-inducible CRISPRa/i systems for rapid and reversible manipulation of gene transcription
- Pro-repair macrophages driven by CGRP rescue white matter integrity following intracerebral hemorrhage
- Mutations in PSEN1 predispose inflammation in an astrocyte model of familial Alzheimer's disease through disrupted regulated intramembrane proteolysis
- 3D Brain Vascular Niche Model Captures Glioblastoma Infiltration, Dormancy, and Gene Signatures
- NRF2 pathway activation predicts poor prognosis in lung cancer: a cautionary note on antioxidant interventions
- Construction and validation of a prognostic model for glioma: an analysis based on mismatch repair-related genes and their correlation with clinicopathological features

The terms “molecular signature” and “gene signature” are often used interchangeably, but they have some distinct differences:

Molecular Signature: A molecular signature refers to a specific pattern or combination of biomolecules that are characteristic of a particular condition, disease, or biological state. The molecular signature can include various types of biomolecules, such as proteins, lipids, metabolites, or even a combination of these. Molecular signatures are often used in biomarker discovery and disease diagnosis, as they can provide valuable insights into the underlying molecular mechanisms and can be used to distinguish between different disease states. Examples of molecular signatures include protein biomarkers, metabolomic profiles, and lipid signatures.

Gene Signature: A gene signature refers to a specific pattern or set of genes that are differentially expressed in a particular condition, disease, or biological state. Gene signatures are typically based on the analysis of gene expression data, such as from microarray or RNA-sequencing experiments. Gene signatures can be used to identify specific molecular pathways or biological processes that are altered in a particular condition, and they can be used for disease classification, prognosis, or treatment selection. Examples of gene signatures include gene expression profiles associated with cancer subtypes, immune cell activation, or drug response. In summary, the key difference is that a molecular signature encompasses a broader range of biomolecules, while a gene signature specifically focuses on the patterns of gene expression. Both molecular and gene signatures can provide valuable insights into the underlying biology and can be used for various applications in biomedical research and clinical practice.

A gene signature or gene expression signature is a single or combined group of genes in a cell with a unique characteristic pattern of gene expression that occurs as a result of an altered or unaltered biological process or pathogenic medical condition.

This is not to be confused with the concept of gene expression profiling. Activating pathways in a regular physiological process or physiological response to a stimulus results in a cascade of signal transduction and interactions that elicit altered levels of gene expression, which is classified as the gene signature of that physiological process or response.

The clinical applications of gene signatures breakdown into prognostic, diagnostic and predictive signatures. The phenotypes that may theoretically be defined by a gene expression signature range from those that predict the survival or prognosis of an individual with a disease, those that are used to differentiate between different subtypes of a disease, to those that predict activation of a particular pathway. Ideally, gene signatures can be used to select a group of patients for whom a particular treatment will be effective.