

CSF methylome

- Epigenome-wide association study of cerebrospinal fluid-based biomarkers of Alzheimer's disease in cognitively normal individuals
- Advancing Personalized Medicine in Alzheimer's Disease: Liquid Biopsy Epigenomics Unveil *APOE* ϵ 4-Linked Methylation Signatures
- Epigenome-wide association study of cerebrospinal fluid-based biomarkers of Alzheimer's disease in cognitively normal individuals
- Blood and cerebrospinal fluid biomarkers in neuro-oncology
- Blood DNA methylomic signatures associated with CSF biomarkers of Alzheimer's disease in the EMIF-AD study
- Establishing the utility of multi-platform liquid biopsy by integrating the CSF methylome and proteome in CNS tumours
- Liquid biopsy in brain tumors: moving on, slowly
- The G9a histone methyltransferase represses osteoclastogenesis and bone resorption by regulating NFATc1 function

The CSF **methylome** refers to the pattern of **DNA methylation**, an epigenetic modification that can affect gene expression, in the cerebrospinal fluid (CSF). The CSF is a clear, colorless fluid that surrounds the brain and spinal cord and provides protection and nourishment for these vital organs. Changes in the CSF methylome have been associated with a variety of neurological and psychiatric conditions, including Alzheimer's disease, Parkinson's disease, multiple sclerosis, and major depressive disorder. DNA methylation patterns in the CSF can be analyzed using advanced sequencing and bioinformatics technologies, and may provide a valuable biomarker for the diagnosis and monitoring of these and other conditions. However, more research is needed to fully understand the role of the CSF methylome in health and disease.

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