

Gene methylation, gene mutations, and protein markers are commonly used biomarkers for brain tumor diagnosis. However, the mechanisms of brain tumorigenesis are complex, and a large number of studies have demonstrated the limitations of relying on single omics, as the analysis of single-level data can only provide little cause-and-effect relationships. In contrast, a multi omics data integration strategy spanning genomic, transcriptomic, proteomic, and metabolomic levels of different cellular functions has the potential to provide unparalleled insights into the underlying biology of brain tumors.