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# When do I ask for a DNA methylation array for primary brain tumor diagnosis?

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## Abstract

**Purpose of review:** Despite remarkable advances in molecular characterization, the diagnosis of brain tumors remains challenging, particularly in cases with ambiguous histology or contradictory molecular features. In this context, DNA methylation profiling plays an important role in improving diagnostic and prognostic accuracy. This review aims to provide diagnostic guidance regarding when DNA methylation arrays represent a useful tool for the diagnosis of primary brain tumors.

**Recent findings:** Large-scale profiling has revealed that DNA methylation profiles of brain tumors are highly reproducible and stable. Therefore, DNA methylation profiling has been successfully used to classify brain tumors and identify new entities. This approach seems to be particularly promising for heterogeneous groups of tumors, such as IDH-wildtype gliomas, and glioneuronal and embryonal tumors, which include a variety of entities that are still under characterization.

**Summary:** As underlined in the fifth edition of the WHO classification of central nervous system tumors, the diagnosis of brain tumors requires the integration of histological, molecular, clinical, and radiological features. Although advanced imaging and histological examination remain the standard diagnostic tools, DNA methylation analysis can significantly improve diagnostic accuracy, with a substantial impact on patient management.

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