

## Proteomic analysis of glioblastomas: what is the best brain control sample?

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**UNLABELLED:** Glioblastoma (GB) is the most frequent and aggressive tumor of the central nervous system. There is currently growing interest in proteomic studies of GB, particularly with the aim of identifying new prognostic or therapeutic response markers. However, comparisons between different proteomic analyses of GB have revealed few common differentiated proteins. The types of control samples used to identify such proteins may in part explain the different results obtained. We therefore tried to determine which control samples would be most suitable for GB proteomic studies. We used an isotope-coded protein labeling (ICPL) method followed by mass spectrometry to reveal and compare the protein patterns of two commonly used types of control sample: GB peritumoral brain zone samples (PBZ) from six patients and epilepsy surgery brain samples (EB) pooled from three patients. The data obtained were processed using AMEN software for network analysis. We identified 197 non-redundant proteins and 35 of them were differentially expressed. Among these 35 differentially expressed proteins, six were over-expressed in PBZ and 29 in EB, showing different proteomic patterns between the two samples. Surprisingly, EB appeared to display a tumoral-like expression pattern in comparison to PBZ. In our opinion, PBZ may be more appropriate control sample for GB proteomic analysis.

**BIOLOGICAL SIGNIFICANCE:** This manuscript describes an original study in which we used an isotope-coded protein labeling method followed by mass spectrometry to identify and compare the protein patterns in two types of sample commonly used as control for glioblastoma (GB) proteomic analysis: peritumoral brain zone and brain samples obtained during surgery for epilepsy. The choice of control samples is critical for identifying new prognostic and/or diagnostic markers in GB.

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## Liens

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