Glioblastoma multiforme (GBM), an aggressive brain tumor, is characterized histologically by the presence of a necrotic center surrounded by so-calledpseudopalisading cells. Pseudopalisading necrosis has long been used as a prognostic feature. However, the underlying molecular mechanism regulating the progression of GBMs remains unclear.

Wang et al., hypothesized that the gene expression profilings of individual cancers, specifically necrosis-related genes, would provide objective information that would allow for the creation of a prognostic index. Gene expression profiles of necrotic and nonnecrotic areas were obtained from the Ivy Glioblastoma Atlas Project (IVY GAP) database to explore the differentially expressed genes.A robust signature of seven genes was identified as a predictor for glioblastoma and low-grade glioma (GBM/LGG) in patients from The Cancer Genome Atlas (TCGA) cohort. This set of genes was able to stratify GBM/LGG and GBM patients into high-risk and low-risk groups in the training set as well as the validation set. The TCGA, Repository for Molecular Brain Neoplasia Data (Rembrandt), and GSE16011 databases were then used to validate the expression level of these seven genes in GBMs and LGGs. Finally, the differentially expressed genes (DEGs) in the high-risk and low-risk groups were subjected to gene ontology enrichment, Kyoto Encyclopedia of Genes and Genomes pathway, and gene set enrichment analyses, and they revealed that these DEGs were associated with immune and inflammatory responses. In conclusion, the study identified a novel seven-gene signature that may guide the prognostic prediction and development of therapeutic applications [1)].

1)
Wang J, Ma J. Integrated Transcriptomic Analysis of Necrosis-related Gene in Diffuse Gliomas. J Neurol Surg A Cent Eur Neurosurg. 2019 Apr 1. doi: 10.1055/s-0039-1683448. [Epub ahead of print] PubMed PMID: 30934097.