

Glioma coexpression analysis

Systemic [coexpression analysis](#) of [glioma](#) could be beneficial for the identification and development of new prognostic and predictive [markers](#) in the clinical management.

Shi et al., from [Hangzhou](#), Department of Neurosurgery, Changhai Hospital, Second Military Medical University, [Shanghai](#). Department of Neurosurgery, Huai'an Second People's Hospital, The Affiliated Huai'an Hospital of Xuzhou Medical University, Huai'an, [China](#), extracted [data sets](#) from the [Gene Expression Omnibus data set](#) by using "glioma" as the keyword. Then, a [coexpression module](#) was constructed with the help of [Weighted Gene Coexpression Network Analysis](#) software. Besides, [Gene Ontology](#) (GO) and [Kyoto Encyclopedia of Genes and Genomes](#) (KEGG) enrichment analyses were performed on the [genes](#) in these modules. As a result, the critical modules and target genes were identified. Eight coexpression modules were constructed using the 4,000 genes with a high expression value of the total 141 glioma samples. The result of the analysis of the interaction among these modules showed that there was a high scale independence degree among them. The GO and KEGG enrichment analyses showed that there was a significant difference in the enriched terms and degree among these eight modules, and module 5 was identified as the most important module. Besides, the pathways it was enriched in, hsa04510: Focal adhesion and hsa04610: Complement and coagulation cascades, were determined as the most important pathways. In summary, module 5 and the pathways it was enriched in, hsa04510: Focal adhesion and has 04610: Complement and coagulation cascades, have the potential to serve as [glioma biomarkers](#) ¹⁾.

¹⁾

Shi T, Chen J, Li J, Yang BY, Zhang QL. Identification of key gene modules and pathways of human glioma through [coexpression network](#). J Cell Physiol. 2018 Aug 1. doi: 10.1002/jcp.27059. [Epub ahead of print] PubMed PMID: 30067869.

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