

Phylogenetic analysis of the tumor-specifically expressed pseudogene ENSG00000186076

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Motivation and Aim: In this paper, we performed a phylogenetic analysis of the non-coding gene ENSG00000186076. This gene is located at chromosome 12 and has been identified as a processed pseudogene of PGAM1 gene. According to Bibert et al, 2021 the ENSG00000186076 gene expression is significantly reduced in a group of patients with severe COVID-19, indicating the level of expression of this gene is associated with the severity of disease. The homologs were searched in 15 genomes of species of the human lineage.

Methods and Algorithms: To proceed analysis and build phylogenetic tree were used full genomes of 15 species, sequence of non-coding gene. We then performed phylogenetic tree reconstruction to examine the evolutionary relationships among the selected sequences using multiple alignment and based on the alignment tree was constructed. For tumor expression analysis, expressions of this gene in different tumors were used.

Results: The phylogenetic tree showed that this gene has a lot of copies or that it's a copy of another. Expression analysis showed reliable differences in tumor expression.

Conclusion: This gene followed our lineage for a long time and presumably has impact on tumor forming.

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References

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