Procollagen C-Endopeptidase Enhancer 2

- Integration of single-cell and bulk RNA sequencing data using machine learning identifies oxidative stress-related genes LUM and PCOLCE2 as potential biomarkers for heart failure
- 2,3,5,4'-tetrahydroxystilbene-2-O-beta-D-glucoside-stimulated dental pulp stem cells-derived exosomes for wound healing and bone regeneration
- Pitavastatin, Procollagen Pathways, and Plaque Stabilization in Patients With HIV: A Secondary Analysis of the REPRIEVE Randomized Clinical Trial
- Quantitative proteomics analysis of cerebrospinal fluid reveals putative protein biomarkers for canine non-infectious meningoencephalomyelitis
- Systemic inhibition of bone morphogenetic protein 1.3 as a possible treatment for laminin-related congenital muscular dystrophy
- PCPE2: Expression of multifunctional extracellular glycoprotein associated with diverse cellular functions
- PCPE-2 (procollagen C-proteinase enhancer-2): The non-identical twin of PCPE-1
- Identification of the Immune-related lncRNA SNHG14/ miR-200a-3p/ PCOLCE2 Axis in Colorectal Cancer

A significant difference was found between primary glioblastoma and glioblastoma recurrence at the transcriptional level. Similar to other omics studies of cancer, a weak overlap was observed between transcriptome and proteome, and Procollagen C-Endopeptidase Enhancer 2 (PCOLCE2) was observed to be upregulated at mRNA and protein levels. Analysis of the public cancer database revealed that high expression of PCOLCE2 is associated with poor prognosis of patients with GBM and that it may be a potential prognostic indicator. Functional and environmental enrichment analyses revealed significantly altered signaling pathways related to energy metabolism, including mitochondrial ATP synthesis-coupled electron transport and oxidative phosphorylation.

This study provides new insights into the recurrence process of GBM through combined transcriptomic and proteomic analyses, complementing the existing GBM transcriptomic and proteomic data and suggesting that integrated multi-omics analyses may reveal new disease features of GBM [1)].

1)

Zhang J, Wang G, Yan B, Yang G, Yang Q, Hu Y, Guo J, Zhao N, Wang L, Wang H. Integrative analysis of transcriptome and proteome profiles in primary and recurrent glioblastoma. Proteomics Clin Appl. 2023 Dec 1:e2200085. doi: 10.1002/prca.202200085. Epub ahead of print. PMID: 38037768.