Resource Summary Report

Generated by RRID on Apr 17, 2025

PseudoFuN

RRID:SCR_017095
Type: Tool

Proper Citation

PseudoFuN (RRID:SCR_017095)

Resource Information

URL: https://integrativeomics.shinyapps.io/pseudofun_app/

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Description: Software as database and query tool for homologous pseudogene and coding gene families. Collection of human pseudogenes and gene associations. Supports search, graphical visualization and functional analysis of pseudogenes and coding genes based on PGG families.

Synonyms: Pseudogene Functional Networks

Resource Type: data analysis service, database, data or information resource, analysis service resource, production service resource, service resource

Keywords: gene, pseudogene, sequence, homology, regulatory, network, miRNA, coexpression, noncoding, RNA, TCGA, cancer

Funding: NLM T15 LM011270

Availability: Free, Freely available

Resource Name: PseudoFuN

Resource ID: SCR_017095

Alternate URLs: https://github.com/yanzhanglab/PseudoFuN_app

License: CC, MIT

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250417T065608+0000

Ratings and Alerts

No rating or validation information has been found for PseudoFuN.

No alerts have been found for PseudoFuN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Pappalardo XG, et al. (2023) Human VDAC pseudogenes: an emerging role for VDAC1P8 pseudogene in acute myeloid leukemia. Biological research, 56(1), 33.

Johnson TS, et al. (2019) PseudoFuN: Deriving functional potentials of pseudogenes from integrative relationships with genes and microRNAs across 32 cancers. GigaScience, 8(5).