Resource Summary Report

Generated by dkNET on May 18, 2025

Tumor Associated Gene database

RRID:SCR_005754
Type: Tool

Proper Citation

Tumor Associated Gene database (RRID:SCR_005754)

Resource Information

URL: http://www.binfo.ncku.edu.tw/TAG/GeneDoc.php

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Description: A database of oncogenes and tumor suppressor genes. Users can search by genes, chromosomes, and keywords. The coAnsensus domain analysis tool functions to identify conserved protein domains and GO terms among selected TAG genes, while the “oncogenic domain analysis” can analyze oncogenic potential of any user-provided protein based on a weighed term frequency table calculated from the TAG proteins. The completion of human genome sequences allows one to rapidly identify and analyze genes of interest through the use of computational approach. The available annotations including physical characterization and functional domains of known tumor-related genes thus can be used to study the role of genes involved in carcinogenesis. The tumor-associated gene (TAG) database was designed to utilize information from well-characterized oncogenes and tumor suppressor genes to facilitate cancer research. All target genes were identified through text-mining approach from the PubMed database. A semi-automatic information retrieving engine was built to collect specific information of these target genes from various resources and store in the TAG database. At current stage, 519 TAGs including 198 oncogenes, 170 tumor suppressor genes, and 151 genes related to oncogenesis were collected. Information collected in TAG database can be browsed through user-friendly web interfaces that provide searching genes by chromosome or by keywords. The “consensus domain analysis” tool functions to identify conserved protein domains and GO terms among selected TAG genes. In addition, the “oncogenic domain analysis” can analyze oncogenic potential of any user-provided protein based on a weighed term frequency table calculated from the TAG proteins. This study was supported by grant from National research program for genomic medicine (NRPGM) and personnel from Bioinformatics Center of Center for Biotechnology and Biosciences in the National Cheng Kung University, Taiwan.

Abbreviations: TAG

Synonyms: Tumor Associated Gene database

Resource Type: database, data or information resource

Funding:

Resource Name: Tumor Associated Gene database

Resource ID: SCR_005754

Alternate IDs: nif-0000-03597

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250517T055719+0000

Ratings and Alerts

No rating or validation information has been found for Tumor Associated Gene database.

No alerts have been found for Tumor Associated Gene database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Mun DG, et al. (2019) Proteogenomic Characterization of Human Early-Onset Gastric Cancer. Cancer cell, 35(1), 111.

Shen H, et al. (2018) Exploring the molecular mechanisms of osteosarcoma by the integrated analysis of mRNAs and miRNA microarrays. International journal of molecular medicine, 42(1), 21.

Chen W, et al. (2016) Potential molecular characteristics in situ in response to repetitive UVB irradiation. Diagnostic pathology, 11(1), 129.

Shen LI, et al. (2016) Identification of genes and signaling pathways associated with squamous cell carcinoma by bioinformatics analysis. Oncology letters, 11(2), 1382.

Huang CH, et al. (2015) Prediction of cancer proteins by integrating protein interaction, domain frequency, and domain interaction data using machine learning algorithms. BioMed research international, 2015, 312047.

Bhatnagar S, et al. (2014) TRIM37 is a new histone H2A ubiquitin ligase and breast cancer oncoprotein. Nature, 516(7529), 116.

Yang J, et al. (2014) Analysis of tumor suppressor genes based on gene ontology and the KEGG pathway. PloS one, 9(9), e107202.

Funk WD, et al. (2012) Evaluating the genomic and sequence integrity of human ES cell lines; comparison to normal genomes. Stem cell research, 8(2), 154.