Resource Summary Report

Generated by RRID on Apr 19, 2025

MedScan

RRID:SCR_003314
Type: Tool

Proper Citation

MedScan (RRID:SCR_003314)

Resource Information

URL: http://www.elsevier.com/online-tools/pathway-studio/biological-database

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 5, 2023. MedScan is a fast and flexible biomedical information extraction technology. It uses dictionaries to identify individual biomedical terms (proteins, cellular processes, small molecules, diseases, etc) referred to in literature articles, and applies advanced natural language processing techniques to detect the relationships within the article and extract these terms and the relationships; the overall process of detection, identification, extraction and assembling, is termed Information Harvesting. Information extracted by MedScan represents the multiple aspects of protein function, including protein modification, cellular localization, protein-protein interactions, gene expression regulation, molecular transport and synthesis, as well as association with diseases, and regulation of various cellular processes. This scope can be broadened by modifying information extraction rules and the dictionaries. Dictionaries can be assembled on any topic or area that is represented in the literature you wish to harvest. High-throughput data generation methodologies like microarray gene expression require new approaches for gathering information for data analysis. For the best results, computational approaches used for high-throughput data analysis require that biological information from the literature be a coherent and integrated part of the analysis software itself. Pathway Studio meets this challenge through its MedScan Technology and underlying ResNet database. All editions of Pathway Studio contain MedScan Technology to harvest information from the literature and to save this information in the Pathway Studio ResNet database ready for data analysis. MedScan is more than a web search engine. Indeed, the output of a Google search can be channeled into MedScan for example. Web searches, like Google, are excellent at finding items as a result of a query. A quick look at the output list usually locates the item for which you are looking. This approach however, is not well suited for information and knowledge gathering. Also, once information is gathered, where do you put it for later computational use? MedScan meets this challenge for the area of biomedical literature and biomedical online information. PubMed meets the needs for a central repository of biomedical literature. Researchers can go to PubMed and search for any topic and articles of interest, much like a web type of search. However, just like a web type of search, PubMed also provides a list of all the hits with a link to the articles. If a single article, or even just a few, are sought, this search approach is useful. Alternatively, MedScan will list all the articles of interest but additionally scans the text for relationships, highlights these relationships in the articles and then lists these relationships and the biological molecules and processes involved in the relationships in separate tables. The tables of relationships can be viewed graphically in Pathway Studio and can be saved into the ResNet database for use in experimental data analysis.

Synonyms: MedScan

Resource Type: data processing software, software application, data acquisition software, software resource

Defining Citation: PMID:15033866

Keywords: expression, function, article, biological, biomedical, cellular, dictionary, disease, information, literature, localization, medline interfaces, modification, molecule, process, protein, regulation, synthesis, technology, term, transport, FASEB list

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MedScan

Resource ID: SCR_003314

Alternate IDs: nif-0000-21259

Old URLs: http://www.ariadnegenomics.com/products/medscan/reader/

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250419T054914+0000

Ratings and Alerts

No rating or validation information has been found for MedScan.

No alerts have been found for MedScan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Bachman JA, et al. (2023) Automated assembly of molecular mechanisms at scale from text mining and curated databases. Molecular systems biology, 19(5), e11325.

Hazi A, et al. (2023) Crosstalk between short- and long-term calorie restriction transcriptomic signatures with anxiety-like behavior, aging, and neurodegeneration: implications for drug repurposing. Frontiers in behavioral neuroscience, 17, 1257881.

Ouni E, et al. (2022) Proteome-wide and matrisome-specific atlas of the human ovary computes fertility biomarker candidates and open the way for precision oncofertility. Matrix biology : journal of the International Society for Matrix Biology, 109, 91.

Long J, et al. (2022) Convergent lines of evidence supporting involvement of NFKB1 in schizophrenia. Psychiatry research, 312, 114588.

Govic A, et al. (2022) Long-Term Calorie Restriction Alters Anxiety-like Behaviour and the Brain and Adrenal Gland Transcriptomes of the Ageing Male Rat. Nutrients, 14(21).

Lim YS, et al. (2021) Descriptive and functional characterization of epidermal growth factor?like domain 8 in mouse cortical thymic epithelial cells by integrated analysis of gene expression signatures and networks. International journal of molecular medicine, 47(3).

Mohammadi-Dehcheshmeh M, et al. (2021) A Transcription Regulatory Sequence in the 5' Untranslated Region of SARS-CoV-2 Is Vital for Virus Replication with an Altered Evolutionary Pattern against Human Inhibitory MicroRNAs. Cells, 10(2).

Sharifi S, et al. (2021) Systems Biology-Derived Genetic Signatures of Mastitis in Dairy Cattle: A New Avenue for Drug Repurposing. Animals : an open access journal from MDPI, 12(1).

Paaso A, et al. (2021) Interferon-? and IL-5 associated cell-mediated immune responses to HPV16 E2 and E6 distinguish between persistent oral HPV16 infections and noninfected mucosa. Clinical and experimental dental research, 7(5), 903.

Yang X, et al. (2021) Schizophrenia Plays a Negative Role in the Pathological Development of Myocardial Infarction at Multiple Biological Levels. Frontiers in genetics, 12, 607690.

Moore NL, et al. (2020) Anti-proliferative transcriptional effects of medroxyprogesterone acetate in estrogen receptor positive breast cancer cells are predominantly mediated by the progesterone receptor. The Journal of steroid biochemistry and molecular biology, 199, 105548.

Prieto M, et al. (2020) Data-driven classification of the certainty of scholarly assertions. PeerJ, 8, e8871.

Morris MC, et al. (2020) Immune Network Modeling Predicts Specific Nasopharyngeal and Peripheral Immune Dysregulation in Otitis-Prone Children. Frontiers in immunology, 11, 1168.

Zhang G, et al. (2019) Cross-disease analysis identified novel common genes for both lung adenocarcinoma and lung squamous cell carcinoma. Oncology letters, 18(4), 3463.

Oh JH, et al. (2018) Whole-genome resequencing and transcriptomic analysis of genes regulating anthocyanin biosynthesis in black rice plants. 3 Biotech, 8(2), 115.

Zhou Y, et al. (2018) Mannose receptor modulates macrophage polarization and allergic inflammation through miR-511-3p. The Journal of allergy and clinical immunology, 141(1), 350.

Alanazi IO, et al. (2018) Computational systems biology analysis of biomarkers in lung cancer; unravelling genomic regions which frequently encode biomarkers, enriched pathways, and new candidates. Gene, 659, 29.

Chiha W, et al. (2018) Retinal genes are differentially expressed in areas of primary versus secondary degeneration following partial optic nerve injury. PloS one, 13(2), e0192348.

Xu C, et al. (2018) Comprehensive literature data-mining analysis reveals a broad genetic network functionally associated with autism spectrum disorder. International journal of molecular medicine, 42(5), 2353.

Li Z, et al. (2018) Integrative computational evaluation of genetic markers for Alzheimer's disease. Saudi journal of biological sciences, 25(5), 996.