Resource Summary Report

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GeneWays: A System for Extracting, Analyzing, Visualizing and Integrating Molecular Pathway Data

RRID:SCR_008368
Type: Tool

Proper Citation

GeneWays: A System for Extracting, Analyzing, Visualizing and Integrating Molecular Pathway Data (RRID:SCR_008368)

Resource Information

URL: http://anya.igsb.anl.gov/Geneways/GeneWays.html

Proper Citation: GeneWays: A System for Extracting, Analyzing, Visualizing and Integrating Molecular Pathway Data (RRID:SCR_008368)

Description: A system for automatically extracting, analyzing, visualizing and integrating molecular pathway data from the research literature. The system focuses on interactions between molecular substances and actions, providing a graphical consensus view on the collected information. GeneWays is designed as an open platform, allowing researchers to query, review and critique the integrated information. Knowledge integration in the domain of molecular biology is crucial for a deeper understanding of molecular cell functions. Integration can be accomplished by gathering research results published in the scientific literature. Unfortunately, researchers are facing a true challenge how to best integrate the sheer amount of scientific publications available. GeneWays is built to help integrating research results by providing automatic tools to gather knowledge from the scientific literature. The GeneWays project team comprises experts from biology, computer science and linguistics, who use natural language processing (NLP) to scan thousands of research articles in order to automatically extract relevant molecular knowledge. The key idea is rather simple: While a single author may be an ultimate expert on a specific molecular substance, the collective knowledge of the whole research community is currently unavailable in an integrated form. Molecular interactions are frequently represented in research articles by statements such as protein A activates protein B, which can be collected and integrated into knowledge about a complex molecular network consisting of thousands of genes, proteins, small molecules (along with other substances) and their interactions. GeneWays's architecture combines various modules designed to automatically gather knowledge on signal transduction pathways from online scientific journals. The core of the system is a knowledge base of molecular actions. The knowledge is provided by various system modules, which select scientific journals of interest, mark and identify substance names in the journal text and extract interactions

between these substances and other actions by means of natural language processing (NLP). The integrated knowledge stored in a database can be queried, analyzed, critiqued and visualized by interested researchers.

Abbreviations: GeneWays

Synonyms: GeneWays: A System for Extracting Analyzing Visualizing and Integrating Molecular Pathway Data, GeneWays: A System for Extracting Analyzing Visualizing Integrating Molecular Pathway Data

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

Defining Citation: PMID:15016385

Keywords: text mining, information extraction, molecular network, molecular interaction, artificial intelligence, knowledge engineering, machine learning, natural language processing

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Resource Name: GeneWays: A System for Extracting, Analyzing, Visualizing and Integrating Molecular Pathway Data

Resource ID: SCR_008368

Alternate IDs: nif-0000-30019

Old URLs: http://anya.igsb.anl.gov/genewaysApp

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260903T234934+0000

Ratings and Alerts

No rating or validation information has been found for GeneWays: A System for Extracting, Analyzing, Visualizing and Integrating Molecular Pathway Data.

No alerts have been found for GeneWays: A System for Extracting, Analyzing, Visualizing and Integrating Molecular Pathway Data.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Selvaraj S, et al. (2023) Diclofenac Disrupts the Circadian Clock and through Complex Cross-Talks Aggravates Immune-Mediated Liver Injury-A Repeated Dose Study in Minipigs for 28 Days. International journal of molecular sciences, 24(2).

Benjamin SJ, et al. (2021) Macrophage mediated recognition and clearance of Borrelia burgdorferi elicits MyD88-dependent and -independent phagosomal signals that contribute to phagocytosis and inflammation. BMC immunology, 22(1), 32.

Ramzan F, et al. (2020) Identification of Age-Specific and Common Key Regulatory Mechanisms Governing Eggshell Strength in Chicken Using Random Forests. Genes, 11(4).

Lee YS, et al. (2020) IL-32? suppressed atopic dermatitis through inhibition of miR-205 expression via inactivation of nuclear factor-kappa B. The Journal of allergy and clinical immunology, 146(1), 156.

Kim KC, et al. (2018) Suppression of metastasis through inhibition of chitinase 3-like 1 expression by miR-125a-3p-mediated up-regulation of USF1. Theranostics, 8(16), 4409.

Lee YS, et al. (2018) Inhibition of skin carcinogenesis by suppression of NF-?B dependent ITGAV and TIMP-1 expression in IL-32? overexpressed condition. Journal of experimental & clinical cancer research : CR, 37(1), 293.

Liu G, et al. (2017) Functional diversity of topological modules in human protein-protein interaction networks. Scientific reports, 7(1), 16199.

Selvaraj S, et al. (2017) The pathogenesis of diclofenac induced immunoallergic hepatitis in a canine model of liver injury. Oncotarget, 8(64), 107763.

Lee EH, et al. (2016) Immunogenomics reveal molecular circuits of diclofenac induced liver injury in mice. Oncotarget, 7(12), 14983.

Mandloi S, et al. (2015) PALM-IST: Pathway Assembly from Literature Mining--an Information Search Tool. Scientific reports, 5, 10021.

Ciribilli Y, et al. (2015) Decoding c-Myc networks of cell cycle and apoptosis regulated genes in a transgenic mouse model of papillary lung adenocarcinomas. Oncotarget, 6(31), 31569.

Malusa F, et al. (2015) Time-course gene profiling and networks in demethylated retinoblastoma cell line. Oncotarget, 6(27), 23688.

Borlak J, et al. (2015) Proteome mapping of epidermal growth factor induced hepatocellular carcinomas identifies novel cell metabolism targets and mitogen activated protein kinase signalling events. BMC genomics, 16(1), 124.

Li X, et al. (2014) Network based integrated analysis of phenotype-genotype data for prioritization of candidate symptom genes. BioMed research international, 2014, 435853.

Hossain MS, et al. (2012) Connecting the dots between PubMed abstracts. PloS one, 7(1), e29509.

Holmes AB, et al. (2011) Discovering disease associations by integrating electronic clinical data and medical literature. PloS one, 6(6), e21132.