Resource Summary Report

Generated by NIF on May 15, 2025

Evex

RRID:SCR_010509
Type: Tool

Proper Citation

Evex (RRID:SCR_010509)

Resource Information

URL: http://evexdb.org

Proper Citation: Evex (RRID:SCR_010509)

Description: EVEX is a text mining resource built on top of PubMed abstracts and PubMed Central full texts. It contains over 40 million bio-molecular events among more than 76 million automatically extracted gene/protein name mentions. The text mining data further has been enriched with gene normalization results, allowing straightforward integration with external resources. Further, gene families from Ensembl and HomoloGene provide homology-based event generalizations. EVEX presents both direct and indirect associations between genes and proteins, enabling explorative browsing of relevant literature.

Resource Type: software application, text-mining software, data or information resource, database, software resource

Keywords: gene, protein, bio.tools

Funding:

Resource Name: Evex

Resource ID: SCR_010509

Alternate IDs: biotools:evex, nlx_158731

Alternate URLs: https://bio.tools/evex

Record Creation Time: 20220129T080259+0000

Record Last Update: 20250514T061537+0000

Ratings and Alerts

No rating or validation information has been found for Evex.

No alerts have been found for Evex.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Hosseinpoor Z, et al. (2024) Crosstalk between MIR-96 and IRS/PI3K/AKT/VEGF cascade in hRPE cells; A potential target for preventing diabetic retinopathy. PloS one, 19(9), e0310999.

Zupi?i? IG, et al. (2022) Is the Illegal Trade of Glass Eels (Anguilla anguilla) Increasing the Spread of Disease? A Case of EVEX. Microorganisms, 10(11).

Lee J, et al. (2020) Literature mining for context-specific molecular relations using multimodal representations (COMMODAR). BMC bioinformatics, 21(Suppl 5), 250.

Weber L, et al. (2020) PEDL: extracting protein-protein associations using deep language models and distant supervision. Bioinformatics (Oxford, England), 36(Suppl_1), i490.

Defoort J, et al. (2019) The Evolution of Gene Duplicates in Angiosperms and the Impact of Protein-Protein Interactions and the Mechanism of Duplication. Genome biology and evolution, 11(8), 2292.

Westergaard D, et al. (2019) Population-wide analysis of differences in disease progression patterns in men and women. Nature communications, 10(1), 666.

D'Cruz OJ, et al. (2018) Impact of targeting transforming growth factor ?-2 with antisense OT-101 on the cytokine and chemokine profile in patients with advanced pancreatic cancer. OncoTargets and therapy, 11, 2779.

Kreula SM, et al. (2018) Finding novel relationships with integrated gene-gene association network analysis of Synechocystis sp. PCC 6803 using species-independent text-mining. PeerJ, 6, e4806.

Wagh K, et al. (2018) Completeness of HIV-1 Envelope Glycan Shield at Transmission Determines Neutralization Breadth. Cell reports, 25(4), 893.

Al-Baghdadi RJT, et al. (2017) Role of activating transcription factor 4 in the hepatic

response to amino acid depletion by asparaginase. Scientific reports, 7(1), 1272.

Mehryary F, et al. (2016) Filtering large-scale event collections using a combination of supervised and unsupervised learning for event trigger classification. Journal of biomedical semantics, 7, 27.

Serin EA, et al. (2016) Learning from Co-expression Networks: Possibilities and Challenges. Frontiers in plant science, 7, 444.

Loviglio MN, et al. (2016) Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. Genome medicine, 8(1), 105.

Venkatesan A, et al. (2016) SciLite: a platform for displaying text-mined annotations as a means to link research articles with biological data. Wellcome open research, 1, 25.

Yu C, et al. (2016) A Physical Mechanism and Global Quantification of Breast Cancer. PloS one, 11(7), e0157422.

Hakala K, et al. (2015) Application of the EVEX resource to event extraction and network construction: Shared Task entry and result analysis. BMC bioinformatics, 16 Suppl 16(Suppl 16), S3.

Prabhu L, et al. (2015) Critical role of phosphorylation of serine 165 of YBX1 on the activation of NF-?B in colon cancer. Oncotarget, 6(30), 29396.

Vanegas JA, et al. (2015) An Overview of Biomolecular Event Extraction from Scientific Documents. Computational and mathematical methods in medicine, 2015, 571381.