

Resource Summary Report

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

Keywords: gene, protein, bio.tools

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: 20260905T132643+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 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hosseinpour 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.

Li S, et al. (2023) Global quantitative understanding of non-equilibrium cell fate decision-making in response to pheromone. iScience, 26(10), 107885.

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 γ -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.

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

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.

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- κ 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.