

Resource Summary Report

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EGAN: Exploratory Gene Association Networks

RRID:SCR_008856

Type: Tool

Proper Citation

EGAN: Exploratory Gene Association Networks (RRID:SCR_008856)

Resource Information

URL: <http://akt.ucsf.edu/EGAN/>

Proper Citation: EGAN: Exploratory Gene Association Networks (RRID:SCR_008856)

Description: Exploratory Gene Association Networks (EGAN) is a software tool that allows a bench biologist to visualize and interpret the results of high-throughput exploratory assays in an interactive hypergraph of genes, relationships (protein-protein interactions, literature co-occurrence, etc.) and meta-data (annotation, signaling pathways, etc.). EGAN provides comprehensive, automated calculation of meta-data coincidence (over-representation, enrichment) for user- and assay-defined gene lists, and provides direct links to web resources and literature (NCBI Entrez Gene, PubMed, KEGG, Gene Ontology, iHOP, Google, etc.). EGAN functions as a module for exploratory investigation of analysis results from multiple high-throughput assay technologies, including but not limited to: * Transcriptomics via expression microarrays or RNA-Seq * Genomics via SNP GWAS or array CGH * Proteomics via MS/MS peptide identifications * Epigenomics via DNA methylation, ChIP-on-Chip or ChIP-Seq * In-silico analysis of sequences or literature EGAN has been built using Cytoscape libraries for graph visualization and layout, and is comparable to DAVID, GSEA, Ingenuity IPA and Ariadne Pathway Studio. There are pre-collated EGAN networks available for human (*Homo sapiens*), mouse (*Mus musculus*), rat (*Rattus norvegicus*), chicken (*Gallus gallus*), zebrafish (*Danio rerio*), fruit fly (*Drosophila melanogaster*), nematode (*Caenorhabditis elegans*), mouse-ear cress (*Arabidopsis thaliana*), rice (*Oryza sativa*) and brewer's yeast (*Saccharomyces cerevisiae*). There is now an EGAN module available for GenePattern (human-only). Platform: Windows compatible, Mac OS X compatible, Linux compatible

Abbreviations: EGAN

Synonyms: Exploratory Gene Association Networks, Exploratory Gene Association Networks (EGAN)

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

Defining Citation: [PMID:19933825](#)

Keywords: gene, gene association, network, protein-protein interaction, pathway, interaction, annotation, signaling pathway, enrichment, cytoscape, visualization

Funding: NCI P30 CA92103

Availability: Free for academic use

Resource Name: EGAN: Exploratory Gene Association Networks

Resource ID: SCR_008856

Alternate IDs: nlx_149222

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260728T043313+0000

Ratings and Alerts

No rating or validation information has been found for EGAN: Exploratory Gene Association Networks.

No alerts have been found for EGAN: Exploratory Gene Association Networks.

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 [nidm-terms](#) .

Hüls A, et al. (2022) Brain DNA Methylation Patterns in CLDN5 Associated With Cognitive Decline. Biological psychiatry, 91(4), 389.

Kudo T, et al. (2020) Constitutive Expression of the Immunosuppressive Tryptophan Dioxygenase TDO2 in Glioblastoma Is Driven by the Transcription Factor C/EBP?. Frontiers in immunology, 11, 657.

Hayrabedyan S, et al. (2019) Synthetic PreImplantation Factor (sPIF) induces posttranslational protein modification and reverses paralysis in EAE mice. Scientific reports, 9(1), 12876.

Ling Y, et al. (2018) Thermoprimer triggers splicing memory in Arabidopsis. Journal of experimental botany, 69(10), 2659.

Hayrabedyan S, et al. (2016) Sertoli cells have a functional NALP3 inflammasome that can modulate autophagy and cytokine production. *Scientific reports*, 6, 18896.

Wang Y, et al. (2016) Proteomic Analysis Implicates Dominant Alterations of RNA Metabolism and the Proteasome Pathway in the Cellular Response to Carbon-Ion Irradiation. *PloS one*, 11(10), e0163896.

Li Z, et al. (2012) Expression profiles of microRNAs from lactating and non-lactating bovine mammary glands and identification of miRNA related to lactation. *BMC genomics*, 13, 731.

Jesmin J, et al. (2010) Gene regulatory network reveals oxidative stress as the underlying molecular mechanism of type 2 diabetes and hypertension. *BMC medical genomics*, 3, 45.