Resource Summary Report

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GOEAST - Gene Ontology Enrichment Analysis Software Toolkit

RRID:SCR_006580
Type: Tool

Proper Citation

GOEAST - Gene Ontology Enrichment Analysis Software Toolkit (RRID:SCR_006580)

Resource Information

URL: http://omicslab.genetics.ac.cn/GOEAST/

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Description: Gene Ontology Enrichment Analysis Software Toolkit (GOEAST) is a web based software toolkit providing easy to use, visualizable, comprehensive and unbiased Gene Ontology (GO) analysis for high-throughput experimental results, especially for results from microarray hybridization experiments. The main function of GOEAST is to identify significantly enriched GO terms among give lists of genes using accurate statistical methods. Compared with available GO analysis tools, GOEAST has the following unique features: * GOEAST supports analysis for data from various resources, such as expression data obtained using Affymetrix, illumina, Agilent or customized microarray platforms. GOEAST also supports non-microarray based experimental data. The web-based feature makes GOEAST very user friendly; users only have to provide a list of genes in correct formats. * GOEAST provides visualizable analysis results, by generating graphs exhibiting enriched GO terms as well as their relationships in the whole GO hierarchy. * Note that GOEAST generates separate graph for each of the three GO categories, namely biological process, molecular function and cellular component. * GOEAST allows comparison of results from multiple experiments (see Multi-GOEAST tool). The displayed color of each GO term node in graphs generated by Multi-GOEAST is the combination of different colors used in individual GOEAST analysis. Platform: Online tool

Abbreviations: GOEAST

Synonyms: Gene Ontology Enrichment Analysis Software Toolkit, Gene Ontology Enrichment Analysis Software Toolkit (GOEAST)

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Defining Citation: PMID:18487275

Keywords: statistical analysis, gene ontology, high-throughput, microarray, hybridization, gene, visualization, bio.tools

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Availability: Free for academic use

Resource Name: GOEAST - Gene Ontology Enrichment Analysis Software Toolkit

Resource ID: SCR_006580

Alternate IDs: biotools:goeast, nlx_149248

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

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Ratings and Alerts

No rating or validation information has been found for GOEAST - Gene Ontology Enrichment Analysis Software Toolkit.

No alerts have been found for GOEAST - Gene Ontology Enrichment Analysis Software Toolkit.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Wang P, et al. (2020) The genome evolution and domestication of tropical fruit mango. Genome biology, 21(1), 60.

Li Y, et al. (2020) Exosomal prostate-specific G-protein-coupled receptor induces osteoblast activity to promote the osteoblastic metastasis of prostate cancer. Translational cancer research, 9(10), 5857.

Sun RZ, et al. (2019) Comparative physiological, metabolomic, and transcriptomic analyses reveal developmental stage-dependent effects of cluster bagging on phenolic metabolism in Cabernet Sauvignon grape berries. BMC plant biology, 19(1), 583.

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Kim MC, et al. (2016) An Integrated Analysis of the Genome-Wide Profiles of DNA Methylation and mRNA Expression Defining the Side Population of a Human Malignant Mesothelioma Cell Line. Journal of Cancer, 7(12), 1668.

Zhang Q, et al. (2016) The chromatin remodeler DDM1 promotes hybrid vigor by regulating salicylic acid metabolism. Cell discovery, 2, 16027.

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Goswami S, et al. (2016) SSH Analysis of Endosperm Transcripts and Characterization of Heat Stress Regulated Expressed Sequence Tags in Bread Wheat. Frontiers in plant science, 7, 1230.

Lima JM, et al. (2015) Physiological, anatomical and transcriptional alterations in a rice mutant leading to enhanced water stress tolerance. AoB PLANTS, 7.