Resource Summary Report

Generated by NIF on Apr 19, 2025

GeneMerge

RRID:SCR_005744
Type: Tool

Proper Citation

GeneMerge (RRID:SCR_005744)

Resource Information

URL: http://www.oeb.harvard.edu/faculty/hartl/old_site/lab/publications/GeneMerge.html

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Description: THIS RESOURCE IS NO LONGER IN SERVCE, documented September 2, 2016. Web-based and standalone application that returns a wide range of functional genomic data for a given set of study genes and provides rank scores for over-representation of particular functions or categories in the data. It uses the hypergeometric test statistic which returns statistically correct results for samples of all sizes and is the #2 fastest GO tool available (Khatri and Draghici, 2005). GeneMerge can be used with any discrete, locus-based annotation data, including, literature references, genetic interactions, mutant phenotypes as well as traditional Gene Ontology queries. GeneMerge is particularly useful for the analysis of microarray data and other large biological datasets. The big advantage of GeneMerge over other similar programs is that you are not limited to analyzing your data from the perspective of a pre-packaged set of gene-association data. You can download or create gene-association files to analyze your data from an unlimited number of perspectives. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: GeneMerge

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

Defining Citation: PMID:12724301

Keywords: gene, genomics, functional genomic data, analysis, post-genomic analysis, data mining, hypothesis testing, statistical analysis, slimmer-type tool, term enrichment, text mining, false discovery rate, bonferroni correction, false discovery rate and bonferroni

correction, perl, microarray

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GeneMerge

Resource ID: SCR_005744

Alternate IDs: nlx_149203

Old URLs: http://genemerge.cbcb.umd.edu/

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250420T015148+0000

Ratings and Alerts

No rating or validation information has been found for GeneMerge.

No alerts have been found for GeneMerge.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Abrusán G, et al. (2024) Cellular location shapes quaternary structure of enzymes. Nature communications, 15(1), 8505.

Abrusán G, et al. (2022) Known allosteric proteins have central roles in genetic disease. PLoS computational biology, 18(2), e1009806.

Morales-Cruz A, et al. (2021) Introgression among North American wild grapes (Vitis) fuels biotic and abiotic adaptation. Genome biology, 22(1), 254.

Haas JC, et al. (2021) Candidate regulators and target genes of drought stress in needles and roots of Norway spruce. Tree physiology, 41(7), 1230.

Ferreira-Neto JRC, et al. (2021) The Cowpea Kinome: Genomic and Transcriptomic Analysis

Under Biotic and Abiotic Stresses. Frontiers in plant science, 12, 667013.

Abrusán G, et al. (2019) Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. Journal of molecular biology, 431(19), 3871.

Abrusán G, et al. (2018) Ligand Binding Site Structure Influences the Evolution of Protein Complex Function and Topology. Cell reports, 22(12), 3265.

Bensaoud C, et al. (2018) De novo assembly and annotation of Hyalomma dromedarii tick (Acari: Ixodidae) sialotranscriptome with regard to gender differences in gene expression. Parasites & vectors, 11(1), 314.

Herron MD, et al. (2018) Genetics of a de novo origin of undifferentiated multicellularity. Royal Society open science, 5(8), 180912.

Zúñiga-León E, et al. (2018) NeVOmics: An Enrichment Tool for Gene Ontology and Functional Network Analysis and Visualization of Data from OMICs Technologies. Genes, 9(12).

Ohkura M, et al. (2018) Comparative Genomics of Aspergillus flavus S and L Morphotypes Yield Insights into Niche Adaptation. G3 (Bethesda, Md.), 8(12), 3915.

He K, et al. (2017) Multiple miRNAs jointly regulate the biosynthesis of ecdysteroid in the holometabolous insects, Chilo suppressalis. RNA (New York, N.Y.), 23(12), 1817.

Kaur P, et al. (2017) Genome-wide identification and characterization of miRNAome from tomato (Solanum lycopersicum) roots and root-knot nematode (Meloidogyne incognita) during susceptible interaction. PloS one, 12(4), e0175178.

Cunha CP, et al. (2017) Ethylene-induced transcriptional and hormonal responses at the onset of sugarcane ripening. Scientific reports, 7, 43364.

Yu X, et al. (2017) Long non-coding RNA Linc-RAM enhances myogenic differentiation by interacting with MyoD. Nature communications, 8, 14016.

Valadez-Cano C, et al. (2017) Natural selection drove metabolic specialization of the chromatophore in Paulinella chromatophora. BMC evolutionary biology, 17(1), 99.

Ferreira SS, et al. (2016) Co-expression network analysis reveals transcription factors associated to cell wall biosynthesis in sugarcane. Plant molecular biology, 91(1-2), 15.

Dong X, et al. (2015) Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. Bioinformatics and biology insights, 9, 61.

Whiston E, et al. (2015) Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. G3 (Bethesda, Md.), 6(2), 235.

Gupta S, et al. (2014) Transcriptome analysis reveals dysregulation of innate immune response genes and neuronal activity-dependent genes in autism. Nature communications, 5, 5748.