

Resource Summary Report

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StRAnGER

RRID:SCR_004247

Type: Tool

Proper Citation

StRAnGER (RRID:SCR_004247)

Resource Information

URL: <http://www.grissom.gr/stranger/>

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Description: StRAnGER (Statistical Ranking of ANotated Genomic Experimental Results) is a web application for the automated statistical analysis of annotated gene profiling experiments, exploiting controlled biological vocabularies, like the Gene Ontology or the KEGG pathways terms. Starting from annotated lists of differentially expressed genes StRAnGER repartitions and reorders the initial distribution of terms to define a new distribution of elements where each element pools terms holding the same enrichment score. The elements are then prioritized according to StRAnGER's algorithm and, by applying bootstrapping techniques, a corrected measure of the statistical significance of these elements is derived, enabling the selection of terms mapped to these elements, unambiguously associated with respective significant gene sets. Besides their high statistical score, another selection criterion for the terms is the number of their members, something that incurs a biological prioritization in line with a Systems Biology context.
Platform: Online tool

Abbreviations: StRAnGER

Synonyms: Statistical Ranking of ANotated Genomic Experimental Results

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

Defining Citation: [PMID:21293737](#)

Keywords: controlled vocabulary, functional analysis, genomics, annotation, visualization, statistical analysis, term enrichment, ontology or annotation visualization

Availability: Free for academic use

Resource Name: StRAnGER

Resource ID: SCR_004247

Alternate IDs: nlx_25932

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260818T043214+0000

Ratings and Alerts

No rating or validation information has been found for StRAnGER.

No alerts have been found for StRAnGER.

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](#) .

Kofman O, et al. (2020) Developmental and social deficits and enhanced sensitivity to prenatal chlorpyrifos in PON1-/- mouse pups and adults. PloS one, 15(9), e0239738.

Koutsandreas T, et al. (2019) ANASTASIA: An Automated Metagenomic Analysis Pipeline for Novel Enzyme Discovery Exploiting Next Generation Sequencing Data. Frontiers in genetics, 10, 469.

Georgiadis P, et al. (2017) Evolving DNA methylation and gene expression markers of B-cell chronic lymphocytic leukemia are present in pre-diagnostic blood samples more than 10??years prior to diagnosis. BMC genomics, 18(1), 728.

Rakitsch B, et al. (2016) Modelling local gene networks increases power to detect trans-acting genetic effects on gene expression. Genome biology, 17, 33.

Papadodima O, et al. (2016) Modulation of Pathways Underlying Distinct Cell Death Mechanisms in Two Human Lung Cancer Cell Lines in Response to SN1 Methylating Agents Treatment. PloS one, 11(7), e0160248.

Spokes AC, et al. (2016) Children's Expectations and Understanding of Kinship as a Social Category. Frontiers in psychology, 7, 440.

Voutetakis K, et al. (2015) Comparative Meta-Analysis of Transcriptomics Data during Cellular Senescence and In Vivo Tissue Ageing. Oxidative medicine and cellular longevity, 2015, 732914.

Hao J, et al. (2015) Latent Fairness in Adults' Relationship-Based Moral Judgments. *Frontiers in psychology*, 6, 1871.

Moon C, et al. (2015) Mothers say "baby" and their newborns do not choose to listen: a behavioral preference study to compare with ERP results. *Frontiers in human neuroscience*, 9, 153.

Visconti di Oleggio Castello M, et al. (2014) Facilitated detection of social cues conveyed by familiar faces. *Frontiers in human neuroscience*, 8, 678.

Pampalakis G, et al. (2014) The KLK5 protease suppresses breast cancer by repressing the mevalonate pathway. *Oncotarget*, 5(9), 2390.

Logotheti M, et al. (2013) A comparative genomic study in schizophrenic and in bipolar disorder patients, based on microarray expression profiling meta-analysis. *TheScientificWorldJournal*, 2013, 685917.

Narayanan NS, et al. (2013) Common medial frontal mechanisms of adaptive control in humans and rodents. *Nature neuroscience*, 16(12), 1888.

Papadodima O, et al. (2013) HuR-regulated mRNAs associated with nuclear hnRNP A1-RNP complexes. *International journal of molecular sciences*, 14(10), 20256.

Johnson SM, et al. (2013) Soothing the threatened brain: leveraging contact comfort with emotionally focused therapy. *PloS one*, 8(11), e79314.

Papadodima O, et al. (2012) Application of an integrative computational framework in transcriptomic data of atherosclerotic mice suggests numerous molecular players. *Advances in bioinformatics*, 2012, 453513.

Chatziioannou AA, et al. (2011) Exploiting Statistical Methodologies and Controlled Vocabularies for Prioritized Functional Analysis of Genomic Experiments: the StRAnGER Web Application. *Frontiers in neuroscience*, 5, 8.

Jimoh A, et al. (2007) Quantifying the economic burden of malaria in Nigeria using the willingness to pay approach. *Cost effectiveness and resource allocation* : C/E, 5, 6.