Resource Summary Report

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FunSpec

RRID:SCR_006952
Type: Tool

Proper Citation

FunSpec (RRID:SCR_006952)

Resource Information

URL: http://funspec.med.utoronto.ca/

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Description: FunSpec is a web-based tool for statistical evaluation of groups of genes and proteins (e.g. co-regulated genes, protein complexes, genetic interactors) with respect to existing annotations, including GO terms. FunSpec (an acronym for Functional Specification) inputs a list of yeast gene names, and outputs a summary of functional classes, cellular localizations, protein complexes, etc. that are enriched in the list. The classes and categories evaluated were downloaded from the MIPS Database and the GO Database . In addition, many published datasets have been compiled to evaluate enrichment against. Hypertext links to the publications are given. The p-values, calculated using the hypergeometric distribution, represent the probability that the intersection of given list with any given functional category occurs by chance. The Bonferroni-correction divides the p-value threshold, that would be deemed significant for an individual test, by the number of tests conducted and thus accounts for spurious significance due to multiple testing over the categories of a database. After the Bonferroni correction, only those categories are displayed for which the chance probability of enrichment is lower than: p-value/#CD where #CD is the number of categories in the selected database. Without the Bonferroni Correction, all categories are displayed for which the same probability of enrichment is lower than: p-value threshold in an individual test Note that many genes are contained in many categories, especially in the MIPS database (which are hierarchical) and that this can create biases for which FunSpec currently makes no compensation. Also the databases are treated as independent from one another, which is really not the case, and each is searched seperately, which may not be optimal for statistical calculations. Nonetheless, we find it useful for sifting through the results of clustering analysis, TAP pulldowns, etc. Platform: Online tool

Abbreviations: FunSpec

Synonyms: Functional Specification

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

Defining Citation: PMID:12431279

Keywords: gene, protein, annotation, gene ontology, gene expression, clustering, prediction, statistical analysis, functional class, cellular localization, protein complex, yeast, FASEB list

Funding: Genome Canada ;
CIHR ;
University of Toronto Connaught Foundation

Availability: Free for academic use

Resource Name: FunSpec

Resource ID: SCR_006952

Alternate IDs: nlx_149246

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250420T015542+0000

Ratings and Alerts

No rating or validation information has been found for FunSpec.

No alerts have been found for FunSpec.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Parisi K, et al. (2024) Hyperpolarisation of Mitochondrial Membranes Is a Critical Component of the Antifungal Mechanism of the Plant Defensin, Ppdef1. Journal of fungi (Basel, Switzerland), 10(1).

Poonia P, et al. (2024) Yeast poly(A)-binding protein (Pab1) controls translation initiation in vivo primarily by blocking mRNA decapping and decay. bioRxiv : the preprint server for biology.

Xiao T, et al. (2024) The phospholipids cardiolipin and phosphatidylethanolamine differentially regulate MDC biogenesis. The Journal of cell biology, 223(5).

Xian J, et al. (2024) Genome-Scale Screening of Saccharomyces cerevisiae Deletion Mutants to Gain Molecular Insight into Tolerance to Mercury Ions. Journal of fungi (Basel, Switzerland), 10(7).

Vijjamarri AK, et al. (2023) Decapping factor Dcp2 controls mRNA abundance and translation to adjust metabolism and filamentation to nutrient availability. eLife, 12.

Mishra PK, et al. (2023) Misregulation of cell cycle-dependent methylation of budding yeast CENP-A contributes to chromosomal instability. Molecular biology of the cell, 34(10), ar99.

Kipanga PN, et al. (2021) Investigating the Antifungal Mechanism of Action of Polygodial by Phenotypic Screening in Saccharomyces cerevisiae. International journal of molecular sciences, 22(11).

Bohm KA, et al. (2021) Distinct roles for RSC and SWI/SNF chromatin remodelers in genomic excision repair. Genome research, 31(6), 1047.

Liu Y, et al. (2021) Stress tolerance enhancement via SPT15 base editing in Saccharomyces cerevisiae. Biotechnology for biofuels, 14(1), 155.

Cao W, et al. (2021) Proteomic analysis revealed the roles of YRR1 deletion in enhancing the vanillin resistance of Saccharomyces cerevisiae. Microbial cell factories, 20(1), 142.

Garcia EJ, et al. (2021) Membrane dynamics and protein targets of lipid droplet microautophagy during ER stress-induced proteostasis in the budding yeast, Saccharomyces cerevisiae. Autophagy, 17(9), 2363.

Sen ND, et al. (2021) Down-Regulation of Yeast Helicase Ded1 by Glucose Starvation or Heat-Shock Differentially Impairs Translation of Ded1-Dependent mRNAs. Microorganisms, 9(12).

Au WC, et al. (2020) Skp, Cullin, F-box (SCF)-Met30 and SCF-Cdc4-Mediated Proteolysis of CENP-A Prevents Mislocalization of CENP-A for Chromosomal Stability in Budding Yeast. PLoS genetics, 16(2), e1008597.

Briz-Cid N, et al. (2020) Influence of tetraconazole on the proteome profile of Saccharomyces cerevisiae Lalvin T73™ strain. Journal of proteomics, 227, 103915.

Brion C, et al. (2020) Pervasive Phenotypic Impact of a Large Nonrecombining Introgressed Region in Yeast. Molecular biology and evolution, 37(9), 2520.

Ganesan S, et al. (2020) Tubular ER Associates With Diacylglycerol-Rich Structures During Lipid Droplet Consumption. Frontiers in cell and developmental biology, 8, 700.

Martínez-Fernández V, et al. (2020) Prefoldin-like Bud27 influences the transcription of ribosomal components and ribosome biogenesis in Saccharomyces cerevisiae. RNA (New York, N.Y.), 26(10), 1360.

Larrimore KE, et al. (2020) Aneuploidy-induced proteotoxic stress can be effectively tolerated without dosage compensation, genetic mutations, or stress responses. BMC biology, 18(1), 117.

Liao PC, et al. (2020) Mitochondria-Associated Degradation Pathway (MAD) Function beyond the Outer Membrane. Cell reports, 32(2), 107902.

Soste M, et al. (2019) Proteomics-Based Monitoring of Pathway Activity Reveals that Blocking Diacylglycerol Biosynthesis Rescues from Alpha-Synuclein Toxicity. Cell systems, 9(3), 309.