Resource Summary Report

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GOEx - Gene Ontology Explorer

RRID:SCR_005779
Type: Tool

Proper Citation

GOEx - Gene Ontology Explorer (RRID:SCR_005779)

Resource Information

URL: http://www.patternlabforproteomics.org/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented July 5, 2018. Gene Ontology Explorer (GOEx) combines data from protein fold changes with GO over-representation statistics to help draw conclusions in proteomic experiments. It is tightly integrated within the PatternLab for Proteomics project and, thus, lies within a complete computational environment that provides parsers and pattern recognition tools designed for spectral counting. GOEx offers three independent methods to query data: an interactive directed acyclic graph, a specialist mode where key words can be searched, and an automatic search. A recent hack included in GOEx is to load the sparse matrix index file directly into GOEx, instead of going through the report generation using the AC/T-fold methods. This makes it easy for GOEx to analyze any list of proteins as long as the list follows the index file format (described in manuscript) . Please note that if using this alternative strategy, there will be no protein fold information. Platform: Windows compatible

Abbreviations: GOEx

Synonyms: Gene Ontology Explorer, GO Explorer

Resource Type: software resource

Defining Citation: PMID:19239707

Keywords: proteomics, visualization, statistical analysis, gene ontology, parse, pattern recognition, spectral counting, analysis, protein fold

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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GOEx - Gene Ontology Explorer

Resource ID: SCR_005779

Alternate IDs: nlx_149249

Old URLs: http://pcarvalho.com/patternlab/goex.shtml

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250410T065331+0000

Ratings and Alerts

No rating or validation information has been found for GOEx - Gene Ontology Explorer.

No alerts have been found for GOEx - Gene Ontology Explorer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

de Oliveira Veloso Rezende J, et al. (2024) A dataset for developing proteomic tools for pathogen detection via differential cell lysis of whole blood samples. Scientific data, 11(1), 1105.

Tarallo D, et al. (2024) Mitofusin 1 silencing decreases the senescent associated secretory

phenotype, promotes immune cell recruitment and delays melanoma tumor growth after chemotherapy. Scientific reports, 14(1), 909.

Brasileiro-Martins LM, et al. (2024) Urinary proteomics reveals biological processes related to acute kidney injury in Bothrops atrox envenomings. PLoS neglected tropical diseases, 18(3), e0012072.

González MJ, et al. (2024) First report on the physicochemical and proteomic characterization of Proteus mirabilis outer membrane vesicles under urine-mimicking growth conditions: comparative analysis with Escherichia coli. Frontiers in microbiology, 15, 1493859.

Ferreira MdS, et al. (2024) ?-1,3-Glucan recognition by Acanthamoeba castellanii as a putative mechanism of amoeba-fungal interactions. Applied and environmental microbiology, 90(2), e0173623.

Camillo-Andrade AC, et al. (2024) Intra-Individual Paired Mass Spectrometry Dataset for Decoding Solar-Induced Proteomic Changes in Facial Skin. Scientific data, 11(1), 441.

Tosar JP, et al. (2022) Exomeres and Supermeres: monolithic or diverse? Journal of extracellular biology, 1(6).

de Lima JY, et al. (2022) Cross-linking mass spectrometry reveals structural insights of the glutamine synthetase from Leishmania braziliensis. Memorias do Instituto Oswaldo Cruz, 116, e210209.

Chalar C, et al. (2021) Embryonic developmental arrest in the annual killifish Austrolebias charrua: A proteomic approach to diapause III. PloS one, 16(6), e0251820.

Bonilauri B, et al. (2021) Proteogenomic Analysis Reveals Proteins Involved in the First Step of Adipogenesis in Human Adipose-Derived Stem Cells. Stem cells international, 2021, 3168428.

González LJ, et al. (2021) Synthesis, LC-MS/MS analysis, and biological evaluation of two vaccine candidates against ticks based on the antigenic P0 peptide from R. sanguineus linked to the p64K carrier protein from Neisseria meningitidis. Analytical and bioanalytical chemistry, 413(23), 5885.

Camillo-Andrade AC, et al. (2020) Proteomics reveals that quinoa bioester promotes replenishing effects in epidermal tissue. Scientific reports, 10(1), 19392.

Silva JM, et al. (2020) Proteomics pinpoints alterations in grade I meningiomas of male versus female patients. Scientific reports, 10(1), 10335.

Tucci P, et al. (2020) Integrative proteomic and glycoproteomic profiling of Mycobacterium tuberculosis culture filtrate. PloS one, 15(3), e0221837.

Macedo-da-Silva J, et al. (2020) Serum Proteomics Reveals Alterations in Protease Activity, Axon Guidance, and Visual Phototransduction Pathways in Infants With In Utero Exposure to

Zika Virus Without Congenital Zika Syndrome. Frontiers in cellular and infection microbiology, 10, 577819.

Brunoro GVF, et al. (2019) Differential proteomic comparison of breast cancer secretome using a quantitative paired analysis workflow. BMC cancer, 19(1), 365.

Losada-Barragán M, et al. (2019) Thymic Microenvironment Is Modified by Malnutrition and Leishmania infantum Infection. Frontiers in cellular and infection microbiology, 9, 252.

Caminha MA, et al. (2019) Trypanosoma cruzi immunoproteome: Calpain-like CAP5.5 differentially detected throughout distinct stages of human Chagas disease cardiomyopathy. Journal of proteomics, 194, 179.

Wippel HH, et al. (2018) Comparing intestinal versus diffuse gastric cancer using a PEFF-oriented proteomic pipeline. Journal of proteomics, 171, 63.

Trugilho MRO, et al. (2017) Platelet proteome reveals novel pathways of platelet activation and platelet-mediated immunoregulation in dengue. PLoS pathogens, 13(5), e1006385.