

Resource Summary Report

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STRAP

RRID:SCR_005675

Type: Tool

Proper Citation

STRAP (RRID:SCR_005675)

Resource Information

URL: <http://www.bumc.bu.edu/cardiovascularproteomics/cpctools/strap/>

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Description: Software program that automatically annotates a protein list with information that helps in the meaningful interpretation of data from mass spectrometry and other techniques. It takes protein lists as input, in the form of plain text files, protXML files (usually from the TPP), or Dat files from MASCOT search results. From this, it generates protein annotation tables, and a variety of GO charts to aid individual and differential analysis of proteomics data. It downloads information from mainly the Uniprot and EBI QuickGO databases. STRAP requires Windows XP or higher with at least version 3.5 of the Microsoft .NET Framework installed. Platform: Windows compatible

Abbreviations: STRAP

Synonyms: Software Tool for Rapid Annotation of Proteins, STRAP for GO Annotation, STRAP - Software Tool for Rapid Annotation of Proteins

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

Defining Citation: [PMID:19839595](#)

Keywords: protein, gene, annotation, mass spectrometry, proteomics, visualization, browser, differential analysis, analysis, ontology or annotation browser, ontology or annotation visualization, differential analysis of proteomics data sets, windows, protein annotation, data visualization, c#, pathway, FASEB list

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NCRR P41 RR10888

Availability: Open unspecified license, Acknowledgement requested

Resource Name: STRAP

Resource ID: SCR_005675

Alternate IDs: OMICS_02277, nlx_149115

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250421T053513+0000

Ratings and Alerts

No rating or validation information has been found for STRAP.

No alerts have been found for STRAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 114 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#).

Carlson RJ, et al. (2024) Single-cell image-based genetic screens systematically identify regulators of Ebola virus subcellular infection dynamics. bioRxiv : the preprint server for biology.

Haddad G, et al. (2024) Identification of Four Mouse FcRn Splice Variants and FcRn-Specific Vesicles. Cells, 13(7).

Kögl T, et al. (2024) Patients and mice with deficiency in the SNARE protein SYNTAXIN-11 have a secondary B cell defect. The Journal of experimental medicine, 221(7).

Kattelus R, et al. (2024) Phenotypic profiling of human induced regulatory T cells at early differentiation: insights into distinct immunosuppressive potential. Cellular and molecular life sciences : CMLS, 81(1), 399.

Yulyaningsih E, et al. (2024) DNL343 is an investigational CNS penetrant eukaryotic initiation factor 2B activator that prevents and reverses the effects of neurodegeneration caused by the integrated stress response. eLife, 12.

Claydon EA, et al. (2024) Detecting sleep and physical activity changes across the perinatal period using wearable technology. *BMC pregnancy and childbirth*, 24(1), 787.

Lin D, et al. (2024) Transcriptome and proteome profiling reveals TREM2-dependent and -independent glial response and metabolic perturbation in an Alzheimer's mouse model. *The Journal of biological chemistry*, 300(11), 107874.

She R, et al. (2023) Translational fidelity screens in mammalian cells reveal eIF3 and eIF4G2 as regulators of start codon selectivity. *Nucleic acids research*, 51(12), 6355.

Lebby R, et al. (2023) The nucleolar protein GNL3 prevents resection of stalled replication forks. *EMBO reports*, 24(12), e57585.

Lorenz-Guertin JM, et al. (2023) Inhibitory and excitatory synaptic neuroadaptations in the diazepam tolerant brain. *Neurobiology of disease*, 185, 106248.

Shuaib M, et al. (2023) Impact of the SARS-CoV-2 nucleocapsid 203K/204R mutations on the inflammatory immune response in COVID-19 severity. *Genome medicine*, 15(1), 54.

Marramà G, et al. (2023) The evolutionary origin of the durophagous pelagic stingray ecomorph. *Palaeontology*, 66(4).

Andersen TO, et al. (2023) Metabolic influence of core ciliates within the rumen microbiome. *The ISME journal*, 17(7), 1128.

Wiciak-Pawłowska K, et al. (2023) The Role of Molecular Structure in Monte Carlo Simulations of the Secondary Electron Yield and Backscattering Coefficient from Methacrylic Acid. *Molecules (Basel, Switzerland)*, 28(3).

Halbout M, et al. (2023) SUZ domain-containing proteins have multiple effects on nonsense-mediated decay target transcripts. *The Journal of biological chemistry*, 299(9), 105095.

Pyrz TW, et al. (2022) Considerations on the Systematics of Neotropical Pierina, with the Description of Two New Species of Phulia Herrich-Schäffer from the Peruvian Andes (Lepidoptera: Pieridae, Pierinae, Pierini). *Neotropical entomology*, 51(6), 840.

Solovieva M, et al. (2022) Disulfiram Oxy-Derivatives Suppress Protein Retrotranslocation across the ER Membrane to the Cytosol and Initiate Paraptosis-like Cell Death. *Membranes*, 12(9).

Platt MP, et al. (2022) A multiomics analysis of direct interkingdom dynamics between influenza A virus and *Streptococcus pneumoniae* uncovers host-independent changes to bacterial virulence fitness. *PLoS pathogens*, 18(12), e1011020.

van de Maat JS, et al. (2021) The influence of chest X-ray results on antibiotic prescription for childhood pneumonia in the emergency department. *European journal of pediatrics*, 180(9), 2765.

Ali S, et al. (2021) Sequence and structure-based method to predict diacylglycerol lipases in

protein sequence. International journal of biological macromolecules, 182, 455.