

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: data processing software, software application, software resource

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

Funding: NHLBI contract N01 HV28178;
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: 20260805T044125+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 120 mentions in open access literature.

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

Fanniel V, et al. (2025) Advancing Soft Tissue Reconstruction with a Ready-to-Use Human Adipose Allograft. Bioengineering (Basel, Switzerland), 12(6).

Huebert DNG, et al. (2025) Coevolution of Lentiviral Vif with Host A3F and A3G: Insights from Computational Modelling and Ancestral Sequence Reconstruction. Viruses, 17(3).

Braunsperger MV, et al. (2025) Proteomic Insights into Human Limbal Epithelial Progenitor-Derived Small Extracellular Vesicles. Stem cell reviews and reports, 21(5), 1578.

Banda NK, et al. (2025) Analysis of human factor H-related gene and protein expressed in rheumatoid arthritis synovium identifies a novel mechanism promoting dysregulated complement pathway activation. Scientific reports, 15(1), 19633.

Lewis MJ, et al. (2025) Deep molecular profiling of synovial biopsies in the STRAP trial identifies signatures predictive of treatment response to biologic therapies in rheumatoid arthritis. Nature communications, 16(1), 5374.

Yan T, et al. (2025) Pigment removal from reverse-printed laminated flexible films by solvent-targeted recovery and precipitation. Science advances, 11(11), eadt5841.

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

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.

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.

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.

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.

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

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.

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).

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.