Resource Summary Report

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BiblioSpec

RRID:SCR_004349
Type: Tool

Proper Citation

BiblioSpec (RRID:SCR_004349)

Resource Information

URL: http://proteome.gs.washington.edu/software/bibliospec/documentation/index.html

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Description: BiblioSpec enables the identification of peptides from tandem mass spectra by searching against a database of previously identified spectra. This suite of software tools is for creating and searching MS/MS peptide spectrum libraries. BiblioSpec is available free of charge for noncommercial use through an interactive web-site at http://depts.washington.edu/ventures/UW_Technology/Express_Licenses/bibliospec.php The BiblioSpec package contains the following programs: * BlibBuild creates a library of peptide MS/MS spectra from MS2 files. * BlibFilter removes redundant spectra from a library. * BlibSearch searches a spectrum library for matches to query spectra, reporting the results in an SQT file. In addition to the primary programs, the following auxiliary programs are available: * BlibStats writes summary statistics describing a library. * BlibToMS2 writes a library in MS2 file format. * BlibUpdate adds, deletes, or annotates spectra. * BlibPpMS2 processes spectra (bins peaks, removes noise, normalizes intensity) as done in BlibSearch and prints the resulting spectra to a text file. Several reference libraries are available for download. These libraries are updated regularly and are for use under the Linux operating system. You will find libraries for * Escherichia coli * Saccharomyces cerevisiae * Caenorhabditis elegans

Resource Type: software resource, data or information resource, database

Defining Citation: PMID:18428681

Funding:

Resource Name: BiblioSpec

Resource ID: SCR_004349

Alternate IDs: nlx_36841

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250410T065152+0000

Ratings and Alerts

No rating or validation information has been found for BiblioSpec.

No alerts have been found for BiblioSpec.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Riley AK, et al. (2024) The deubiquitinase USP9X regulates RIT1 protein abundance and oncogenic phenotypes. iScience, 27(8), 110499.

Soh WT, et al. (2024) Protein degradation by human 20S proteasomes elucidates the interplay between peptide hydrolysis and splicing. Nature communications, 15(1), 1147.

Leibiger TM, et al. (2024) Quantitative proteomic analysis of residual host cell protein retention across adeno-associated virus affinity chromatography. Molecular therapy. Methods & clinical development, 32(4), 101383.

Lou R, et al. (2023) Benchmarking commonly used software suites and analysis workflows for DIA proteomics and phosphoproteomics. Nature communications, 14(1), 94.

Fels U, et al. (2023) Shift in vacuolar to cytosolic regime of infecting Salmonella from a dual proteome perspective. PLoS pathogens, 19(8), e1011183.

Lopez J, et al. (2023) The ribosomal S6 kinase 2 (RSK2)-SPRED2 complex regulates the phosphorylation of RSK substrates and MAPK signaling. The Journal of biological chemistry, 299(6), 104789.

Zinzius K, et al. (2023) Calredoxin regulates the chloroplast NADPH-dependent thioredoxin reductase in Chlamydomonas reinhardtii. Plant physiology, 193(3), 2122.

Hirschberg Y, et al. (2023) Proteomic comparison between non-purified cerebrospinal fluid and cerebrospinal fluid-derived extracellular vesicles from patients with Alzheimer's, Parkinson's and Lewy body dementia. Journal of extracellular vesicles, 12(12), e12383.

Kotimoole CN, et al. (2023) Development of a Spectral Library for the Discovery of Altered Genomic Events in Mycobacterium avium Associated With Virulence Using Mass Spectrometry-Based Proteogenomic Analysis. Molecular & cellular proteomics : MCP, 22(5), 100533.

Wang SY, et al. (2021) Role of epigenetics in unicellular to multicellular transition in Dictyostelium. Genome biology, 22(1), 134.

Willems P, et al. (2021) Use of Hybrid Data-Dependent and -Independent Acquisition Spectral Libraries Empowers Dual-Proteome Profiling. Journal of proteome research, 20(2), 1165.

Mast N, et al. (2021) Brain Acetyl-CoA Production and Phosphorylation of Cytoskeletal Proteins Are Targets of CYP46A1 Activity Modulation and Altered Sterol Flux. Neurotherapeutics : the journal of the American Society for Experimental NeuroTherapeutics, 18(3), 2040.

Jiang L, et al. (2020) A Quantitative Proteome Map of the Human Body. Cell, 183(1), 269.

Low JKK, et al. (2020) The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. Cell reports, 33(9), 108450.

Liang J, et al. (2020) Piperlongumine Acts as an Immunosuppressant by Exerting Prooxidative Effects in Human T Cells Resulting in Diminished TH17 but Enhanced Treg Differentiation. Frontiers in immunology, 11, 1172.

Chanthick C, et al. (2019) Cellular proteome datasets of human endothelial cells under physiologic state and after treatment with caffeine and epigallocatechin-3-gallate. Data in brief, 25, 104292.

Roux-Dalvai F, et al. (2019) Fast and Accurate Bacterial Species Identification in Urine Specimens Using LC-MS/MS Mass Spectrometry and Machine Learning. Molecular & cellular proteomics : MCP, 18(12), 2492.

Chanthick C, et al. (2019) Comparative proteomics reveals concordant and discordant biochemical effects of caffeine versus epigallocatechin-3-gallate in human endothelial cells. Toxicology and applied pharmacology, 378, 114621.

Chollet ME, et al. (2018) Factor VII deficiency: Unveiling the cellular and molecular mechanisms underlying three model alterations of the enzyme catalytic domain. Biochimica et biophysica acta. Molecular basis of disease, 1864(3), 660.

Müller F, et al. (2018) On the Reproducibility of Label-Free Quantitative Cross-Linking/Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 29(2), 405.