

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

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>

Proper Citation: BiblioSpec (RRID:SCR_004349)

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: data or information resource, software resource, database

Defining Citation: [PMID:18428681](#)

Resource Name: BiblioSpec

Resource ID: SCR_004349

Alternate IDs: nlx_36841

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260731T042658+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 29 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Joun GL, et al. (2025) Histone methyltransferase PRDM9 promotes survival of drug-tolerant persister cells in glioblastoma. *Nature communications*, 16(1), 10905.

Lambrechts LS, et al. (2025) The BRD4-nucleosome interaction is enhanced modestly and non-selectively by histone acetylation. *Nucleic acids research*, 53(22).

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

Edgington RM, et al. (2024) Mass Spectral Feature Analysis of Ubiquitylated Peptides Provides Insights into Probing the Dark Ubiquitylome. *Journal of the American Society for Mass Spectrometry*, 35(12), 2849.

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.