Resource Summary Report

Generated by NIF on May 16, 2025

PeptideShaker

RRID:SCR_002520
Type: Tool

Proper Citation

PeptideShaker (RRID:SCR_002520)

Resource Information

URL: https://code.google.com/p/peptide-shaker/

Proper Citation: PeptideShaker (RRID:SCR_002520)

Description: Software providing a search engine independent platform for visualization of peptide and protein identification results from multiple search engines, currently supporting X!Tandem, MS-GF+, MS Amanda, OMSSA, MyriMatch, Comet, Tide, Mascot and mzIdentML. By combining the results from multiple search engines, while re-calculating PTM localization scores and redoing the protein inference, PeptideShaker attempts to give you the best possible understanding of your proteomics data.

Resource Type: software resource

Defining Citation: PMID:34709836

Keywords: standalone software, proteomics, mass spectrometry, java, search engine, omssa, xtandem, mascot, ms-gf, msamanda, myrimatch, comet, tide

Funding:

Availability: Apache License, v2

Resource Name: PeptideShaker

Resource ID: SCR_002520

Alternate IDs: OMICS_03347

Alternate URLs: http://peptide-shaker.googlecode.com

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250420T014108+0000

Ratings and Alerts

No rating or validation information has been found for PeptideShaker.

No alerts have been found for PeptideShaker.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 153 mentions in open access literature.

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

Do K, et al. (2024) A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. mSphere, 9(6), e0079323.

Bertino F, et al. (2024) Dysregulation of FLVCR1a-dependent mitochondrial calcium handling in neural progenitors causes congenital hydrocephalus. Cell reports. Medicine, 5(7), 101647.

Hus KK, et al. (2024) Venom diversity in Naja mossambica: Insights from proteomic and immunochemical analyses reveal intraspecific differences. PLoS neglected tropical diseases, 18(4), e0012057.

Moreno-Tortolero RO, et al. (2024) Molecular organization of fibroin heavy chain and mechanism of fibre formation in Bombyx mori. Communications biology, 7(1), 786.

Nasr E, et al. (2024) microGalaxy: A gateway to tools, workflows, and training for reproducible and FAIR analysis of microbial data. bioRxiv : the preprint server for biology.

Chen R, et al. (2024) HDX-MS finds that partial unfolding with sequential domain activation controls condensation of a cellular stress marker. Proceedings of the National Academy of Sciences of the United States of America, 121(13), e2321606121.

Kruk ME, et al. (2024) An integrated metaproteomics workflow for studying host-microbe dynamics in bronchoalveolar lavage samples applied to cystic fibrosis disease. mSystems, 9(7), e0092923.

Garge RK, et al. (2024) Systematic profiling of ale yeast protein dynamics across fermentation and repitching. G3 (Bethesda, Md.), 14(3).

Deveryshetty J, et al. (2023) C-terminus induced asymmetry within a Rad52 homodecamer dictates single-position Rad51 nucleation in homologous recombination. bioRxiv : the preprint server for biology.

Elliff J, et al. (2023) Dynamic states of eIF6 and SDS variants modulate interactions with uL14 of the 60S ribosomal subunit. Nucleic acids research, 51(4), 1803.

Skiadopoulou D, et al. (2023) Retention Time and Fragmentation Predictors Increase Confidence in Identification of Common Variant Peptides. Journal of proteome research, 22(10), 3190.

Leblanc S, et al. (2023) Newfound Coding Potential of Transcripts Unveils Missing Members of Human Protein Communities. Genomics, proteomics & bioinformatics, 21(3), 515.

Canderan J, et al. (2023) MetaProD: A Highly-Configurable Mass Spectrometry Analyzer for Multiplexed Proteomic and Metaproteomic Data. Journal of proteome research, 22(2), 442.

Kim KS, et al. (2023) Genome-wide multi-omics analysis reveals the nutrient-dependent metabolic features of mucin-degrading gut bacteria. Gut microbes, 15(1), 2221811.

Nabi A, et al. (2023) Discovering misannotated lncRNAs using deep learning training dynamics. Bioinformatics (Oxford, England), 39(1).

Beslic D, et al. (2023) Comprehensive evaluation of peptide de novo sequencing tools for monoclonal antibody assembly. Briefings in bioinformatics, 24(1).

Chaiyadet S, et al. (2023) Small extracellular vesicles but not microvesicles from Opisthorchis viverrini promote cell proliferation in human cholangiocytes. bioRxiv : the preprint server for biology.

van Leeuwen SJM, et al. (2023) The salivary proteome in relation to oral mucositis in autologous hematopoietic stem cell transplantation recipients: a labelled and label-free proteomics approach. BMC oral health, 23(1), 460.

Roshan P, et al. (2023) An Aurora B-RPA signaling axis secures chromosome segregation fidelity. Nature communications, 14(1), 3008.

Garge RK, et al. (2023) Systematic Profiling of Ale Yeast Protein Dynamics across Fermentation and Repitching. bioRxiv : the preprint server for biology.