

Resource Summary Report

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PeptideShaker

RRID:SCR_002520

Type: Tool

Proper Citation

PeptideShaker (RRID:SCR_002520)

Resource Information

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

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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

Availability: Free, Available for download, Freely available

Resource Name: PeptideShaker

Resource ID: SCR_002520

Alternate IDs: OMICS_03347

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

License: Apache License, v2

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260801T190150+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 160 mentions in open access literature.

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

Sadaow L, et al. (2025) Immunomics-guided biomarker discovery for human liver fluke infection and infection-associated cholangiocarcinoma. *Nature communications*, 16(1), 5965.

Vlasov PA, et al. (2025) Multiple human enhancer RNAs contain long translated open reading frames. *Genes & development*, 39(23-24), 1468.

Pipart J, et al. (2025) MultiStageSearch: An Iterative Workflow for Unbiased Taxonomic Analysis of Pathogens Using Proteogenomics. *Journal of proteome research*, 24(6), 2643.

Kaiser A, et al. (2025) Transient ligand contacts of the intrinsically disordered N-terminus of neuropeptide Y2 receptor regulate arrestin-3 recruitment. *Nature communications*, 16(1), 8326.

Wang S, et al. (2025) An Approach to Integrate Metagenomics, Metatranscriptomics and Metaproteomics Data in Public Data Resources. *Proteomics*, 25(17-18), 33.

Meurs J, et al. (2025) High-Throughput Analysis of Protein Adsorption to a Large Library of Polymers Using Liquid Extraction Surface Analysis-Tandem Mass Spectrometry (LESA-MS/MS). *Analytical chemistry*, 97(24), 12776.

Šoi? D, et al. (2025) High-Throughput Site-Specific N-Glycosylation Profiling of Human Fibrinogen in Atrial Fibrillation. *Journal of proteome research*, 24(4), 2121.

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.

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

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.

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*.

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.