

Resource Summary Report

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Data independent acquisition proteomics workbench

RRID:SCR_021862

Type: Tool

Proper Citation

Data independent acquisition proteomics workbench (RRID:SCR_021862)

Resource Information

URL: <https://usegalaxy.eu>

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Description: Software tools for analysis of data independent acquisition type proteomics data are implemented in Galaxy framework. Enables complete DIA data analysis including spectral library generation based on DDA type data, analysis of DIA data in raw or mzml format, and differential statistical analysis. All tools are based on open-source software such as diypasef, OpenSwath, swath2stats and MSstats.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.1101/2021.07.21.453197](https://doi.org/10.1101/2021.07.21.453197)

Keywords: data independent acquisition, proteomics data, Galaxy framework,

Availability: Free, Freely available

Resource Name: Data independent acquisition proteomics workbench

Resource ID: SCR_021862

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Ratings and Alerts

No rating or validation information has been found for Data independent acquisition proteomics workbench.

No alerts have been found for Data independent acquisition proteomics workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 268 mentions in open access literature.

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

Souza LHB, et al. (2025) New Insights into the Sex Chromosome Evolution of the Common Barker Frog Species Complex (Anura, Leptodactylidae) Inferred from Its Satellite DNA Content. *Biomolecules*, 15(6).

Chaity SC, et al. (2025) Genomic characterization and comparative analysis of antibiotic resistance and virulence in Bangladeshi and global *Klebsiella pneumoniae* ST48 strains. *Journal, genetic engineering & biotechnology*, 23(3), 100557.

Delaleau M, et al. (2025) Comprehensive mapping of transcription terminator Rho utilization (Rut) sites across the *Bacillus subtilis* genome. *Nucleic acids research*, 53(15).

Lengyel M, et al. (2025) Zymogen granule protein 16B (ZG16B) is a druggable epigenetic target to modulate the mammary extracellular matrix. *Cancer science*, 116(1), 81.

Denis J, et al. (2025) Identification of *Toxoplasma gondii* antigenic proteins using an in vivo approach and in silico investigation of their polymorphism. *Microbiology spectrum*, 13(5), e0204024.

Wess M, et al. (2025) Versatile roles of annexin A4 in clear cell renal cell carcinoma: Impact on membrane repair, transcriptional signatures, and composition of the tumor microenvironment. *iScience*, 28(4), 112198.

Breidenbach JD, et al. (2025) Microcystin-LR aerosol exposure increases inflammatory drivers of asthma, Evidence of an NF- κ B amplification mechanism. *bioRxiv : the preprint server for biology*.

Sherwood OL, et al. (2025) Transcriptional signatures associated with waterlogging stress responses and aerenchyma formation in barley root tissue. *Annals of botany*, 136(5-6), 1175.

Galindo-Moreno M, et al. (2025) Aurora B and INCENP co-overexpression severely disrupts mitosis and distinctly modifies the global transcriptional landscape. *iScience*, 28(6), 112731.

Casella V, et al. (2025) Novel Insights into the Nobilamide Family from a Deep-Sea *Bacillus*: Chemical Diversity, Biosynthesis and Antimicrobial Activity Towards Multidrug-Resistant Bacteria. *Marine drugs*, 23(1).

Kunz L, et al. (2025) Avirulence depletion assay: Combining R gene-mediated selection with bulk sequencing for rapid avirulence gene identification in wheat powdery mildew. *PLoS pathogens*, 21(1), e1012799.

Banar M, et al. (2025) A novel broad-spectrum bacteriophage cocktail against methicillin-resistant *Staphylococcus aureus*: Isolation, characterization, and therapeutic potential in a mastitis mouse model. *PloS one*, 20(1), e0316157.

Asadi S, et al. (2025) Exploring effector candidates in *Rhynchosporium commune*: insights into their expression dynamics during barley infection. *Scientific reports*, 15(1), 17667.

Triggiano F, et al. (2025) Clinical and environmental investigation of six cases of *Chryseobacterium arthrosphaerae* infections in a Southern Italian hospital. *Scientific reports*, 15(1), 39814.

Soumia PS, et al. (2025) Unravelling the complete mitochondrial genomes of *Thrips tabaci* Lindeman and *Thrips parvispinus* Karny (Thysanoptera: Thripidae) and their phylogenetic implications. *Frontiers in insect science*, 5, 1536160.

Nortje NQ, et al. (2025) Molecular modelling and experimental validation of mangiferin and its related compounds as quorum sensing modulators of *Pseudomonas aeruginosa*. *Archives of microbiology*, 207(3), 53.

Baei B, et al. (2025) Pharmacophore modeling and QSAR analysis of anti-HBV flavonols. *PloS one*, 20(1), e0316765.

Galvis J, et al. (2025) Using DIMet for Differential Analysis of Labeled Metabolomics Data: A Step-by-step Guide Showcasing the Glioblastoma Metabolism. *Bio-protocol*, 15(2), e5168.

Joshi P, et al. (2025) Insights into urinary catheter colonisation and polymicrobial biofilms of *Candida*- bacteria under flow condition. *Scientific reports*, 15(1), 15375.

Wu J, et al. (2025) Genome analysis of colistin-resistant *Salmonella* isolates from human sources in Guizhou of southwestern China, 2019-2023. *Frontiers in microbiology*, 16, 1498995.