

# Resource Summary Report

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## Data independent acquisition proteomics workbench

RRID:SCR\_021862

Type: Tool

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### Proper Citation

Data independent acquisition proteomics workbench (RRID:SCR\_021862)

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### Resource Information

**URL:** <https://usegalaxy.eu>

**Proper Citation:** Data independent acquisition proteomics workbench (RRID:SCR\_021862)

**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 resource, software toolkit

**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,

**Funding:**

**Availability:** Free, Freely available

**Resource Name:** Data independent acquisition proteomics workbench

**Resource ID:** SCR\_021862

**Record Creation Time:** 20220129T080357+0000

**Record Last Update:** 20250422T060228+0000

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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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 192 mentions in open access literature.

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

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.

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.

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).

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.

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.

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

Petroll R, et al. (2025) Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. *The Plant journal : for cell and molecular biology*, 121(1), e17184.

Hermawaty D, et al. (2025) De novo transcriptome assembly and analysis during agarwood induction in *Gyrinops versteegii* Gilg. seedling. *Scientific reports*, 15(1), 2977.

Strateva TV, et al. (2025) First Detection and Genomic Characterization of Linezolid-Resistant *Enterococcus faecalis* Clinical Isolates in Bulgaria. *Microorganisms*, 13(1).

Shaikh MA, et al. (2025) StCDF1: A 'jack of all trades' clock output with a central role in

regulating potato nitrate reduction activity. *The New phytologist*, 245(1), 282.

Zhang N, et al. (2025) Deciphering the molecular logic of WOX5 function in the root stem cell organizer. *The EMBO journal*, 44(1), 281.

Dawson RA, et al. (2025) Carbon monoxide-oxidising Pseudomonadota on volcanic deposits. *Environmental microbiome*, 20(1), 12.

Fracalvieri R, et al. (2025) Isolation and Characterization of Colistin-Resistant Enterobacteriaceae from Foods in Two Italian Regions in the South of Italy. *Microorganisms*, 13(1).

Sageman-Furnas K, et al. (2024) Detailing Early Shoot Growth Arrest in Kro-0 x BG-5 Hybrids of *Arabidopsis thaliana*. *Plant & cell physiology*, 65(3), 420.

Nugroho A, et al. (2024) Transcriptome dataset of gall-rust infected Sengon (*Falcataria falcata*) seedlings using long-read PCR-cDNA sequencing. *Data in brief*, 52, 109919.

de Souza YPA, et al. (2024) The seeds of *Plantago lanceolata* comprise a stable core microbiome along a plant richness gradient. *Environmental microbiome*, 19(1), 11.

Beerling DJ, et al. (2024) Enhanced weathering in the US Corn Belt delivers carbon removal with agronomic benefits. *Proceedings of the National Academy of Sciences of the United States of America*, 121(9), e2319436121.

Thompson RM, et al. (2024) Draft genome sequences of two *Micromonospora* strains isolated from the root nodules of *Alnus glutinosa*. *Microbiology resource announcements*, 13(3), e0113123.

Vieira Da Cruz A, et al. (2024) Pyridylpiperazine efflux pump inhibitor boosts in vivo antibiotic efficacy against *K. pneumoniae*. *EMBO molecular medicine*, 16(1), 93.

Nguyen DH, et al. (2024) Genomic characterization and identification of candidate genes for putative podophyllotoxin biosynthesis pathway in *Penicillium herquei* HGN12.1C. *Microbial biotechnology*, 17(9), e70007.