

# 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,

**Availability:** Free, Freely available

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

**Resource ID:** SCR\_021862

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

**Record Last Update:** 20260912T200259+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 441 mentions in open access literature.

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

Li Y, et al. (2026) Genomic characterization of *Actinobacillus pleuropneumoniae* serovars 5, 8, and 15 strains from diseased pigs in eastern Chinese provinces. *Virulence*, 17(1), 2620200.

Han HJ, et al. (2026) Nontyphoidal *Salmonella* encephalopathy in a teenager from Hubei, China. *Infectious medicine*, 5(1), 100233.

Lv M, et al. (2026) First report of mitochondrial genome of *Cloeon viridulum* (Ephemeroptera: Baetidae) from Hebei, China. *Mitochondrial DNA. Part B, Resources*, 11(1), 74.

Silago V, et al. (2026) Genomic epidemiology of extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* in Mwanza, Tanzania. *Journal of global antimicrobial resistance*, 47, 55.

Yamamoto S, et al. (2026) Dorsoventral-mediated Shh induction is required for axolotl limb regeneration. *eLife*, 14.

Solomon CU, et al. (2026) Integrative functional genomics analysis identifies pleiotropic genes for vascular diseases. *Nature communications*, 17(1).

Badra-Fajardo N, et al. (2026) FANCD2 restrains fork progression and prevents fragility at early origins upon re-replication. *Nature communications*, 17(1).

Rubio T, et al. (2026) Combinations of colistin and bacteriocins prevent the selection of colistin resistance in *Acinetobacter baumannii*. *Communications biology*, 9(1).

Park NH, et al. (2026) Trans-histone crosstalk establishes distinct H3K79 methylation zones with differential transcriptional functions. *Nucleic acids research*, 54(6).

Putra A, et al. (2026) Comprehensive mitogenomic insights into *Hemibagrus velox* endemic to Sumatra, Indonesia and its phylogenetic relationships within the Bagridae lineage. *BMC genomics*, 27(1).

Sayahi N, et al. (2026) Genomic insights into *Serratia bockelmanii* strain 201: unlocking its potential for plant growth promotion and salt stress tolerance. *BMC microbiology*, 26(1).

Famakinde DO, et al. (2026) Dietary variations drive divergent phenotypic, transcriptomic, and metatranscriptomic profiles in *Biomphalaria glabrata*, a schistosomiasis vector snail.

Parasites & vectors, 19(1).

Sirotnina EA, et al. (2026) Evolution of gene order in mtDNA of Baikal endemic amphipods and its possible mechanisms. *Vavilovskii zhurnal genetiki i selektsii*, 30(1), 136.

Weksler NC, et al. (2026) Toxin resistance in the monarch butterfly expanded its milkweed host range. *bioRxiv : the preprint server for biology*.

Pezzi PH, et al. (2026) Chromosome-Level Reference Genome of the Beach False Foxglove, *Agalinis fasciculata* (Orobanchaceae). *Genome biology and evolution*, 18(5).

Li WQ, et al. (2026) The analysis of mitochondrial genome and new distribution of the invasive pest, *Leptoglossus occidentalis* (Heidemann, 1910). *Mitochondrial DNA. Part B, Resources*, 11(6), 739.

Wu G, et al. (2026) An mTORC2-Lipid Signaling Axis Controls Stress-Induced Organismal Death. *Research square*.

Simayi R, et al. (2026) Rocking-induced sleep enhancement promotes motor learning through transcriptional and synaptic remodelling. *Communications biology*, 9(1).

Czarota P, et al. (2026) ICMT deficiency ameliorates weight loss and mortality, but not tumor formation in a mouse model of liver cancer. *Cell communication and signaling : CCS*, 24(1).

Michniewski S, et al. (2026) Rolling out Plaque-2-seq: a single plaque sequencing approach enabling rapid, low-cost sequencing of phages directly from plaques. *Microbial genomics*, 12(4).