

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 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

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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 441 mentions in open access literature.

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

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).

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.

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.

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).

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

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).

Sirotinina 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.

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

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.

Rivarola M, et al. (2026) Chromosome-scale genome assembly of the South American fruit fly, *Anastrepha fraterculus* sp.1. *Insect science*, 33(2), 640.

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

Farajeen H, et al. (2026) Genetic Diversity of *Neospora Caninum* in Palestinian Cattle and Sheep: Insights From Nc-5 Gene Detection and MS10 Microsatellite Analysis. *Veterinary medicine and science*, 12(1), e70811.

González-Peña R, et al. (2026) Characterization of the Bacteriome of *Culicoides reevesi* from Chihuahua, Northern Mexico: Symbiotic and Pathogenic Associations. *Insects*, 17(1).