

Resource Summary Report

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DIA-NN

RRID:SCR_022865

Type: Tool

Proper Citation

DIA-NN (RRID:SCR_022865)

Resource Information

URL: <https://github.com/vdemichev/DiaNN>

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Description: Software tool for processing of data independent acquisition proteomics experiments. Universal automated software suite for DIA proteomics data analysis. Neural networks and interference correction enable deep proteome coverage in high throughput.

Resource Type: software application, data analysis software, software resource, data processing software, time-series analysis software, 2d time-series analysis software

Defining Citation: [PMID:3176806](#)

Keywords: Neural networks, interference correction, data independent acquisition proteomics experiments, DIA proteomics data analysis

Availability: Free, Available for download, Freely available

Resource Name: DIA-NN

Resource ID: SCR_022865

License URLs: <https://github.com/vdemichev/DiaNN/blob/master/LICENSE.txt>

Record Creation Time: 20221013T050144+0000

Record Last Update: 20260729T044547+0000

Ratings and Alerts

No rating or validation information has been found for DIA-NN.

No alerts have been found for DIA-NN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 225 mentions in open access literature.

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

Saschin L, et al. (2026) Antioxidants rescue murine mesangial cells from docosaheptaenoic acid-induced ferroptosis. *Molecular and cellular pediatrics*, 13(1), 2.

Bastrup JA, et al. (2026) Temporal Proteomic Remodeling of Cerebral Arteries in Male Hypertensive Rats. *Hypertension (Dallas, Tex. : 1979)*, 83(1), 73.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. *Molecular cell*, 85(1), 24.

Egawa M, et al. (2025) Generation of Monosomy 21q Human iPS Cells by CRISPR/Cas9-Mediated Interstitial Megabase Deletion. *Genes to cells : devoted to molecular & cellular mechanisms*, 30(1), e13184.

Prakash A, et al. (2025) Integrated View of Baseline Protein Expression in Human Tissues Using Public Data Independent Acquisition Data Sets. *Journal of proteome research*, 24(2), 685.

Park BJ, et al. (2025) CUT&Tag Identifies Repetitive Genomic Loci that are Excluded from ChIP Assays. *bioRxiv : the preprint server for biology*.

Boi R, et al. (2025) Cytoskeleton-associated protein 4 affects podocyte cytoskeleton dynamics in diabetic kidney disease. *JCI insight*, 10(14).

Griesbaum L, et al. (2025) The HL-60 clone 15 cell line as a model for leukocyte migration-possibilities and limitations. *Frontiers in immunology*, 16, 1515993.

Liu YK, et al. (2025) Multiplexed Data-Independent Acquisition (mDIA) to Profile Extracellular Vesicle Proteomes. *bioRxiv : the preprint server for biology*.

Haines M, et al. (2025) High-Throughput Proteomic and Phosphoproteomic Analysis of Formalin-Fixed Paraffin-Embedded Tissues. *Molecular & cellular proteomics : MCP*, 24(9), 101044.

Salovska B, et al. (2025) A robust multiplex-DIA workflow profiles protein turnover regulations associated with cisplatin resistance and aneuploidy. *Nature communications*, 16(1), 5034.

Berg MD, et al. (2025) Mistranslating tRNA variants impact the proteome and phosphoproteome of *Saccharomyces cerevisiae*. *bioRxiv : the preprint server for biology*.

Zheng X, et al. (2025) Integrated multi-omics reveals the molecular mechanism of antibiotic-free Wenchang chicken (*Gallus Gallus domesticus*). *Poultry science*, 104(11), 105801.

Nix MN, et al. (2025) A Bivalent Molecular Glue Linking Lysine Acetyltransferases to Oncogene-induced Cell Death. *bioRxiv : the preprint server for biology*.

Nissen P, et al. (2025) Proteomic Landscape of Colorectal Cancer Derived Liver Metastasis Reveals Three Distinct Phenotypes With Specific Signaling and Enhanced Survival. *Molecular & cellular proteomics : MCP*, 24(8), 101026.

Li X, et al. (2025) Spatial isotope deep tracing deciphers inter-tissue metabolic crosstalk. *Nature communications*, 16(1), 7934.

Zamore M, et al. (2025) Considerations and Software for Successful Immune Cell Deconvolution Using Proteomics Data. *Journal of proteome research*, 24(8), 3751.

Waschbüsch D, et al. (2025) Structural basis for binding of RILPL1 to TMEM55B reveals a lysosomal platform for adaptor assembly through a conserved TBM motif. *bioRxiv : the preprint server for biology*.

Karakosta C, et al. (2025) Comparative Proteomic Analysis of Aqueous Humor, Anterior Lens Capsules, and Crystalline Lenses in Different Human Cataract Subtypes Versus Healthy Controls. *Proteomes*, 13(4).

Wang Z, et al. (2025) Cross-platform clinical proteomics using the Charité open standard for plasma proteomics (OSPP). *Nature communications*, 16(1), 11377.