

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: 2d time-series analysis software, data analysis software, data processing software, software application, software resource, 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: 20260829T182811+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 345 mentions in open access literature.

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

Berg MD, et al. (2026) Mistranslating tRNA variants impact the proteome and phosphoproteome of *Saccharomyces cerevisiae*. *G3* (Bethesda, Md.), 16(2).

Raschdorf A, et al. (2026) Colonic spatial single-cell proteomics and murine models link mitochondrial dysfunction to dimeric IgA-secreting plasma cell deficiency in Crohn's disease. *Nature communications*, 17(1), 1590.

Yu Z, et al. (2026) Spectronaut and DIA-NN: A Comparison of their Performance in the Analysis of Lung Adenocarcinoma Biopsies. *ACS omega*, 11(5), 8080.

Guzman UH, et al. (2026) Higher-Throughput Proteome Profiling Enabled by Parallelized Pre-Accumulation and Optimized Ion Processing in the Orbitrap Astral Zoom Mass Spectrometer. *Molecular & cellular proteomics : MCP*, 25(2), 101504.

Xu N, et al. (2026) Plasma Proteomic Profiling Was Used to Discover a Biochemical Recurrence Prediction Model for Prostate Cancer. *Molecular & cellular proteomics : MCP*, 25(7), 101568.

Snieszek C, et al. (2026) Serum proteomics reveals distinct phenotypic signatures to IL-6 blockade between two immunotherapies. *bioRxiv : the preprint server for biology*.

Arad D, et al. (2026) Landscape and dynamics of TadA-dependent RNA editing in *Escherichia coli* reveal a role in nutrient-rich growth. *mBio*, 17(5), e0055126.

Gao H, et al. (2026) Systematic evaluation of blood contamination in nanoparticle-based plasma proteomics. *EMBO molecular medicine*, 18(1), 275.

Nijssen TI, et al. (2026) Spatial protein expression patterns across pathologically-associated fibers revealed molecular specialization in inclusion body myositis. *Cell communication and signaling : CCS*, 24(1).

Garcia VE, et al. (2026) Evaluating isoprenol production using the IPP-bypass pathway in the oleaginous yeast *Rhodospiridium toruloides*. *Biotechnology for biofuels and bioproducts*, 19(1).

Ananthapadmanabhan V, et al. (2026) Targeted degradation of MDM2 overcomes feedback regulation of p53 signaling in Merkel cell carcinoma models. *The Journal of clinical investigation*, 136(13).

Yang Y, et al. (2026) Elucidating the therapeutic efficacy and mechanisms of arctigenin in ameliorating renal fibrosis: a combined transcriptomic and proteomic study. *Frontiers in*

pharmacology, 17, 1796732.

Glennie L, et al. (2026) The Contribution of Native Protein Complexes to Targeted Protein Degradation. *ACS chemical biology*, 21(5), 1095.

Askin B, et al. (2026) IgLON5 autoimmune antibodies activate Tau via neuronal hyperactivity. *Science advances*, 12(20), eaec2042.

Regina A, et al. (2026) Cardiolipin preserves Treg metabolic fitness and immune homeostasis in the gut. *Nature metabolism*, 8(6), 1368.

Xu T, et al. (2026) Pathogenic mechanism of the PLS1 gene variant in hearing loss and functional validation in a zebrafish model. *Scientific reports*, 16(1).

Graff S, et al. (2026) Histone succinylation directly inhibits Jumonji domain demethylases and stabilizes repressive chromatin states. *bioRxiv : the preprint server for biology*.

Tesfamariam YM, et al. (2026) Poxvirus dsDNA genomes differentially activate AIM2 or NLRP3 inflammasomes in human primary cells. *The EMBO journal*, 45(5), 1728.

Li K, et al. (2026) High-throughput peptide-centric local stability assay extends protein-ligand identification to membrane proteins, tissues and bacteria. *Nature structural & molecular biology*, 33(1), 184.

Grimmer G, et al. (2026) Unlocking the Zn-enriching potential of industrial yeast strains-an experimental journey from metal analysis to proteomics. *Applied microbiology and biotechnology*, 110(1), 12.