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, time-series analysis software, data analysis software, software application, software resource, data processing software

Defining Citation: PMID:3176806

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

Funding:

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: 20250420T015237+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 98 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

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.

Verma S, et al. (2025) The MADS-box protein SHATTERPROOF 2 regulates TAA1 expression in the gynoecium valve margins. Plant reproduction, 38(1), 6.

Zhang C, et al. (2025) Proteomic analysis across aged tissues reveals distinct signatures and the crucial involvement of midgut barrier function in the regulation of aging. Aging cell, 24(1), e14344.

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.

Weber M, et al. (2025) Transcriptomic and proteomic profiling identifies feline fibrosarcoma as clinically amenable model for aggressive sarcoma subtypes. Neoplasia (New York, N.Y.), 60, 101104.

Niroomand A, et al. (2024) Proteomic Analysis of Primary Graft Dysfunction in Porcine Lung Transplantation Reveals Alveolar-Capillary Barrier Changes Underlying the High Particle Flow Rate in Exhaled Breath. Transplant international : official journal of the European Society for Organ Transplantation, 37, 12298. Nurmi K, et al. (2024) Truncating NFKB1 variants cause combined NLRP3 inflammasome activation and type I interferon signaling and predispose to necrotizing fasciitis. Cell reports. Medicine, 5(4), 101503.

Raffo-Romero A, et al. (2024) A co-culture system of macrophages with breast cancer tumoroids to study cell interactions and therapeutic responses. Cell reports methods, 4(6), 100792.

Shukla A, et al. (2024) The Tumor Suppressor SOCS1 Diminishes Tolerance to Oxidative Stress in Hepatocellular Carcinoma. Cancers, 16(2).

Suresh PS, et al. (2024) Spatial Proteomics Reveals Alcohol-Induced Damages to the Crypts and Villi of the Mouse Small Intestine. Journal of proteome research, 23(5), 1801.

Liu X, et al. (2024) A mitochondrial surveillance mechanism activated by SRSF2 mutations in hematologic malignancies. The Journal of clinical investigation, 134(12).

Yamazaki T, et al. (2024) Human RP105 monoclonal antibody enhances antigen-specific antibody production in unique culture conditions. iScience, 27(9), 110649.

Zhuang Z, et al. (2024) Discovery of electrophilic degraders that exploit SNAr chemistry. bioRxiv : the preprint server for biology.

Zhao N, et al. (2024) An Orai1 gain-of-function tubular aggregate myopathy mouse model phenocopies key features of the human disease. The EMBO journal, 43(23), 5941.

Chowdhury MMH, et al. (2024) Impact of a tailored exercise regimen on physical capacity and plasma proteome profile in post-COVID-19 condition. Frontiers in physiology, 15, 1416639.

Salovska B, et al. (2024) A Comprehensive and Robust Multiplex-DIA Workflow Profiles Protein Turnover Regulations Associated with Cisplatin Resistance. bioRxiv : the preprint server for biology.

Chen X, et al. (2024) Integrative metabolomics and proteomics reveal the effect and mechanism of Zi Qi decoction on alleviating liver fibrosis. Scientific reports, 14(1), 28943.

Gaither KA, et al. (2024) Effects of alcohol consumption and tobacco smoking on the composition of the ensemble of drug metabolizing enzymes and transporters in human liver. bioRxiv : the preprint server for biology.

Zhuang X, et al. (2024) Molecular Responses of Anti-VEGF Therapy in Neovascular Age-Related Macular Degeneration: Integrative Insights From Multi-Omics and Clinical Imaging. Investigative ophthalmology & visual science, 65(10), 24.