Resource Summary Report

Generated by RRID on Apr 11, 2025

NetworKIN

RRID:SCR_007818
Type: Tool

Proper Citation

NetworKIN (RRID:SCR_007818)

Resource Information

URL: http://networkin.info/

Proper Citation: NetworKIN (RRID:SCR_007818)

Description: A method for predicting in vivo kinase-substrate relationships, that augments consensus motifs with context for kinases and phosphoproteins. This website allows a user to browse/search and investigate predictions made using the NetworKIN algorithm. The site is powered by the latest phosphoproteome in Phospho.ELM. Alternatively users can submit their own protein sequences and phosphorylation sites and obtain new NetworKIN predictions.

Synonyms: NetworKIN

Resource Type: data or information resource, database

Keywords: FASEB list

Funding:

Resource Name: NetworKIN

Resource ID: SCR_007818

Alternate IDs: nif-0000-03190

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250410T065627+0000

Ratings and Alerts

No rating or validation information has been found for NetworKIN.

No alerts have been found for NetworKIN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 101 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Wang Z, et al. (2025) NEAT1 regulates BMSCs aging through disruption of FGF2 nuclear transport. Stem cell research & therapy, 16(1), 30.

Li F, et al. (2025) Phosphoproteomics profiling of sorafenib-resistant hepatocellular carcinoma patient-derived xenografts reveals potential therapeutic strategies. iScience, 28(1), 111657.

Zhang Q, et al. (2025) Integrated proteogenomic characterization of ampullary adenocarcinoma. Cell discovery, 11(1), 2.

Bhuiyan P, et al. (2024) System biology approaches to identify hub genes linked with ECM organization and inflammatory signaling pathways in schizophrenia pathogenesis. Heliyon, 10(3), e25191.

Li L, et al. (2024) Comprehensive Proteogenomic Profiling Reveals the Molecular Characteristics of Colorectal Cancer at Distinct Stages of Progression. Cancer research, 84(17), 2888.

Park S, et al. (2024) Suppression of Glioblastoma Stem Cell Potency and Tumor Growth via LRRK2 Inhibition. International journal of stem cells, 17(3), 319.

Zou J, et al. (2024) iProPhos: A Web-Based Interactive Platform for Integrated Proteome and Phosphoproteome Analysis. Molecular & cellular proteomics : MCP, 23(1), 100693.

Offenhäuser C, et al. (2024) EphA2 regulates vascular permeability and prostate cancer metastasis via modulation of cell junction protein phosphorylation. Oncogene.

Leung TCN, et al. (2024) Temporal Quantitative Proteomic and Phosphoproteomic Profiling of SH-SY5Y and IMR-32 Neuroblastoma Cells during All-Trans-Retinoic Acid-Induced Neuronal Differentiation. International journal of molecular sciences, 25(2).

Runnebohm AM, et al. (2024) IB-DNQ and Rucaparib dual treatment alters cell cycle regulation and DNA repair in triple negative breast cancer cells. bioRxiv : the preprint server

for biology.

Muneer G, et al. (2024) A Rapid One-Pot Workflow for Sensitive Microscale Phosphoproteomics. Journal of proteome research, 23(8), 3294.

Rebak AS, et al. (2024) A quantitative and site-specific atlas of the citrullinome reveals widespread existence of citrullination and insights into PADI4 substrates. Nature structural & molecular biology, 31(6), 977.

Liu X, et al. (2024) Activation of GPR81 by lactate drives tumour-induced cachexia. Nature metabolism, 6(4), 708.

Yoon KA, et al. (2024) Proteogenomic analysis dissects early-onset breast cancer patients with prognostic relevance. Experimental & molecular medicine, 56(11), 2382.

Li S, et al. (2023) Integrative proteomic characterization of adenocarcinoma of esophagogastric junction. Nature communications, 14(1), 778.

Li L, et al. (2023) Comprehensive proteogenomic characterization of early duodenal cancer reveals the carcinogenesis tracks of different subtypes. Nature communications, 14(1), 1751.

Hu GS, et al. (2023) CPPA: A Web Tool for Exploring Proteomic and Phosphoproteomic Data in Cancer. Journal of proteome research, 22(2), 368.

Shi W, et al. (2023) Multilevel proteomic analyses reveal molecular diversity between diffuse-type and intestinal-type gastric cancer. Nature communications, 14(1), 835.

Li L, et al. (2023) Integrative proteogenomic characterization of early esophageal cancer. Nature communications, 14(1), 1666.

Mancini M, et al. (2023) SETD2 non genomic loss of function in advanced systemic mastocytosis is mediated by an Aurora kinase A/MDM2 axis and can be therapeutically targeted. Biomarker research, 11(1), 29.