

Resource Summary Report

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NetworkKIN

RRID:SCR_007818

Type: Tool

Proper Citation

NetworkKIN (RRID:SCR_007818)

Resource Information

URL: <http://networkkin.info/>

Proper Citation: NetworkKIN (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 NetworkKIN 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 NetworkKIN predictions.

Synonyms: NetworkKIN

Resource Type: data or information resource, database

Keywords: FASEB list

Resource Name: NetworkKIN

Resource ID: SCR_007818

Alternate IDs: nif-0000-03190

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260829T183014+0000

Ratings and Alerts

No rating or validation information has been found for NetworkKIN.

No alerts have been found for NetworkKIN.

Data and Source Information

Usage and Citation Metrics

We found 112 mentions in open access literature.

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

Dunphy K, et al. (2026) Phosphoproteomic Profiling of Multiple Myeloma Based on Ex Vivo Drug Sensitivity Resistance Testing Identifies Phosphorylation Signatures Associated with Drug Response. *Biomolecules*, 16(2).

Xu S, et al. (2026) Proteogenomic Characterization Reveals Subtype-Specific Therapeutic Potential for HER2-Low Breast Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(12), e13086.

Qian P, et al. (2026) Time-of-day effects on post-exercise phosphoproteomic profiling in mouse hippocampus. *Frontiers in cell and developmental biology*, 14, 1788597.

Vijayan J, et al. (2026) Co-Phosphoregulatory Network Underlying Functional Coherence of TLK1 and TLK2 Kinase Paralogs. *International journal of molecular sciences*, 27(12).

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

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

Müller-Dott S, et al. (2025) Comprehensive evaluation of phosphoproteomic-based kinase activity inference. *Nature communications*, 16(1), 4771.

Buttigieg MM, et al. (2025) Inflammatory reprogramming of the solid tumor microenvironment by infiltrating clonal hematopoiesis is associated with adverse outcomes. *Cell reports. Medicine*, 6(3), 101989.

Sigaud R, et al. (2025) Multi-omics dissection of MAPK-driven senescence unveils therapeutic vulnerabilities in KIAA1549::BRAF-fusion pediatric low-grade glioma models. *Signal transduction and targeted therapy*, 10(1), 197.

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

Zhang H, et al. (2025) Nuclear FGF2 orchestrates phase separation-mediated rDNA chromatin architecture to control BMSCs cell fate. *Bone research*, 13(1), 80.

Díez P, et al. (2025) Tonic signaling of the B-cell antigen-specific receptor is a common functional hallmark in chronic lymphocytic leukemia cell phosphoproteomes at early disease stages. *Molecular oncology*, 19(12), 3706.

Pan Z, et al. (2025) Integrative proteogenomic characterization reveals therapeutic targets in poorly differentiated and anaplastic thyroid cancers. *Nature communications*, 16(1), 3601.

Portugal CC, et al. (2025) Profilin 1 controls a microglial cytoskeleton checkpoint to prevent senescence and premature synaptic decline. *Journal of neuroinflammation*, 22(1), 264.

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.

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.

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

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

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).