Resource Summary Report

Generated by NIF on May 13, 2025

PhosphoNET

RRID:SCR_013070
Type: Tool

Proper Citation

PhosphoNET (RRID:SCR_013070)

Resource Information

URL: http://www.phosphonet.ca/

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Description: PhosphoNET is an open-access, online knowledgebase developed by Kinexus Bioinformatics Corporation to foster the study of cell signaling systems to advance biomedical research in academia and industry. PhosphoNET is the world''s largest repository of known and predicted information on human phosphorylation sites, their evolutionary conservation and the identities of protein kinases that may target these sites. Search by protein name, UniProt number, IPI number, or 15 AA P-site sequence. PhosphoNET presently holds data on over 650,000 known and putative phosphorylation sites (P-sites) in over 23,000 human proteins that have been collected from the scientific literature and other reputable websites. Over 14% of these phospho-sites have been experimentally validated. The rest have been predicted with a novel P-Site Predictor algorithm developed at Kinexus with academic partners at the University of British Columbia and Simon Fraser University. With the PhosphoNET Evolution module, this website also provides information about cognate proteins in over 20 other species that may share these human phospho-sites. This helps to define the most functionally important phospho-sites as these are expected to be highly conserved in nature. With the Kinase Predictor module, listings are provided for the top 50 human protein kinases that are likely to phosphorylate each of these phospho-sites using another proprietary kinase substrate prediction algorithm developed at Kinexus. Our kinase substrate predictions are based on deduced consensus phosphorylation site amino acid frequency scoring matrices that we have determined for each of ~500 different human protein kinases. The specificity matrices are generated directly from the primary amino acid sequences of the catalytic domains of these kinases, and when available, have proven to correlate strongly with substrate prediction matrices based on alignment of known substrates of these kinases. The higher the score, the better the prospect that a kinase will phosphorylate a given site. Over 30 million kinase-substrate phospho-site pairs are quantified in PhosphoNET. Kinexus Bioinformatics Corporation has the capability to test most of these putative interactions in vitro for our clients.

Synonyms: PhosphoNET - Human Phospho-Site KnowledgeBase

Resource Type: data or information resource, database, service resource

Keywords: FASEB list

Funding: National Research Council of Canada Industrial Assistance Program ;
Natural Sciences and Engineering Research Council of Canada

Resource Name: PhosphoNET

Resource ID: SCR_013070

Alternate IDs: nlx_98420

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250513T061427+0000

Ratings and Alerts

No rating or validation information has been found for PhosphoNET.

No alerts have been found for PhosphoNET.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 92 mentions in open access literature.

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

Oosterwijk-Wakka JC, et al. (2025) Kinomic profiling to predict sunitinib response of patients with metastasized clear cell Renal Cell Carcinoma. Neoplasia (New York, N.Y.), 60, 101108.

Stefanova D, et al. (2024) FGF receptor kinase inhibitors exhibit broad antiviral activity by targeting Src family kinases. Cellular and molecular life sciences : CMLS, 81(1), 471.

Liu Y, et al. (2024) Phosphorylated FOXQ1, a novel substrate of JNK1, inhibits sorafenib-induced ferroptosis by activating ETHE1 in hepatocellular carcinoma. Cell death & disease, 15(6), 395.

Zhang Y, et al. (2024) TrkA promotes MDM2-mediated AGPS ubiquitination and degradation to trigger prostate cancer progression. Journal of experimental & clinical cancer research : CR, 43(1), 16.

Dollet L, et al. (2024) Exercise-induced crosstalk between immune cells and adipocytes in humans: Role of oncostatin-M. Cell reports. Medicine, 5(1), 101348.

Foster J, et al. (2024) Lipid- and phospho-regulation of CTP:Phosphocholine Cytidylyltransferase ? association with nuclear lipid droplets. Molecular biology of the cell, 35(3), ar33.

Lee CJ, et al. (2024) ELK3 destabilization by speckle-type POZ protein suppresses prostate cancer progression and docetaxel resistance. Cell death & disease, 15(4), 274.

Lopez-Mejia IC, et al. (2023) Oxidative stress-induced FAK activation contributes to uterine serous carcinoma aggressiveness. Molecular oncology, 17(1), 98.

Aguilan JT, et al. (2023) Proteomics and phosphoproteomics profiling in glutamatergic neurons and microglia in an iPSC model of Jansen de Vries Syndrome. bioRxiv : the preprint server for biology.

Fisch D, et al. (2023) PIM1 controls GBP1 activity to limit self-damage and to guard against pathogen infection. Science (New York, N.Y.), 382(6666), eadg2253.

Xiao J, et al. (2023) Control of human pancreatic beta cell kinome by glucagon-like peptide-1 receptor biased agonism. Diabetes, obesity & metabolism, 25(8), 2105.

Esmaili F, et al. (2023) A Review of Machine Learning and Algorithmic Methods for Protein Phosphorylation Site Prediction. Genomics, proteomics & bioinformatics, 21(6), 1266.

Fan Y, et al. (2022) ERK1/2 inhibits Cullin 3/SPOP-mediated PrLZ ubiquitination and degradation to modulate prostate cancer progression. Cell death and differentiation, 29(8), 1611.

Migliavacca J, et al. (2022) Cooperation of Striatin 3 and MAP4K4 promotes growth and tissue invasion. Communications biology, 5(1), 795.

Liang W, et al. (2022) Zinc finger C3H1-type containing serves as a novel prognostic biomarker in human pan-cancer. Gene, 820, 146251.

Che L, et al. (2022) Intracellular antibody targeting HBx suppresses invasion and metastasis in hepatitis B virus-related hepatocarcinogenesis via protein phosphatase 2A-B56?-mediated dephosphorylation of protein kinase B. Cell proliferation, 55(11), e13304.

Barnhart MD, et al. (2022) Phosphorylation of the smooth muscle master splicing regulator RBPMS regulates its splicing activity. Nucleic acids research, 50(20), 11895.

Collins HE, et al. (2022) Cardiomyocyte stromal interaction molecule 1 is a key regulator of

Ca2+ -dependent kinase and phosphatase activity in the mouse heart. Physiological reports, 10(4), e15177.

Cao Y, et al. (2022) A pan-cancer analysis confirms PTPN11's potential as a prognostic and immunological biomarker. Aging, 14(13), 5590.

Xia H, et al. (2022) Insulin action and resistance are dependent on a GSK3?-FBXW7-ERR? transcriptional axis. Nature communications, 13(1), 2105.