Resource Summary Report

Generated by ASWG on Aug 3, 2026

PhosphoPOINT

RRID:SCR_002109
Type: Tool

Proper Citation

PhosphoPOINT (RRID:SCR_002109)

Resource Information

URL: http://kinase.bioinformatics.tw/

Proper Citation: PhosphoPOINT (RRID:SCR_002109)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. A comprehensive human kinase interactome and phospho-protein database. PhosphoPOINT also annotates any amino acids near the phosphorylation sites where a cSNP may cause a phosphorylation site to be lost, and at the same time identifies how such alteration of the phosphorylation site may lead to human disease. PhosphoPOINT integrates 4,195 phospho-proteins, 518 serine/threonine/tyrosine kinases, and their corresponding PPI datasets with the goal of delineating the interactions among kinases, their potential substrates and their interacting (phospho)-proteins. PhosphoPOINT has integrated human protein kinases, phospho-proteins, and PPI datasets with the goal to delineate four kinds of links among kinases. These include their interacting proteins, substrates, and substrates as well as interacting phospho-proteins. Some of these interacting proteins for kinases are phospho-proteins, which might have the potential to serve as substrates for the interacting kinases.

Synonyms: PhosphoPOINT

Resource Type: database, data or information resource

Defining Citation: PMID:18689816

Keywords: amino acid, human disease, human kinase, interactome, phospho-protein, phosphorylation, protein

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PhosphoPOINT

Resource ID: SCR_002109

Alternate IDs: nif-0000-20888

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260803T040314+0000

Ratings and Alerts

No rating or validation information has been found for PhosphoPOINT.

No alerts have been found for PhosphoPOINT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

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

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.

Tang S, et al. (2024) Proteomic characterization identifies clinically relevant subgroups of soft tissue sarcoma. Nature communications, 15(1), 1381.

Zhang Q, et al. (2024) Proteogenomic characterization of skull-base chordoma. Nature communications, 15(1), 8338.

Xiang H, et al. (2024) Proteogenomic insights into the biology and treatment of pan-melanoma. Cell discovery, 10(1), 78.

Yao Z, et al. (2023) Proteogenomics of different urothelial bladder cancer stages reveals distinct molecular features for papillary cancer and carcinoma in situ. Nature communications, 14(1), 5670.

Wang Y, et al. (2023) Proteogenomics of diffuse gliomas reveal molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. Nature communications, 14(1), 505.

Roy-Luzarraga M, et al. (2022) Suppression of Endothelial Cell FAK Expression Reduces Pancreatic Ductal Adenocarcinoma Metastasis after Gemcitabine Treatment. Cancer research, 82(10), 1909.

Badodi S, et al. (2021) Inositol treatment inhibits medulloblastoma through suppression of epigenetic-driven metabolic adaptation. Nature communications, 12(1), 2148.

Heydt Q, et al. (2021) Adipocytes disrupt the translational programme of acute lymphoblastic leukaemia to favour tumour survival and persistence. Nature communications, 12(1), 5507.

Chen CW, et al. (2020) GasPhos: Protein Phosphorylation Site Prediction Using a New Feature Selection Approach with a GA-Aided Ant Colony System. International journal of molecular sciences, 21(21).

Alli-Shaik A, et al. (2017) Phosphoproteomics reveals network rewiring to a pro-adhesion state in annexin-1-deficient mammary epithelial cells. Breast cancer research : BCR, 19(1), 132.

Lehmann S, et al. (2017) Functional phosphatome requirement for protein homeostasis, networked mitochondria, and sarcomere structure in C.??elegans muscle. Journal of cachexia, sarcopenia and muscle, 8(4), 660.

Gao Y, et al. (2016) PredPhos: an ensemble framework for structure-based prediction of phosphorylation sites. Journal of biological research (Thessalonike, Greece), 23(Suppl 1), 12.

Zhang XD, et al. (2016) The exploration of network motifs as potential drug targets from post-translational regulatory networks. Scientific reports, 6, 20558.

Domanova W, et al. (2016) Unraveling Kinase Activation Dynamics Using Kinase-Substrate Relationships from Temporal Large-Scale Phosphoproteomics Studies. PloS one, 11(6), e0157763.

Park JM, et al. (2015) Integrated analysis of global proteome, phosphoproteome, and glycoproteome enables complementary interpretation of disease-related protein networks. Scientific reports, 5, 18189.

Nizard P, et al. (2014) Integrative analysis of high-throughput RNAi screen data identifies the FER and CRKL tyrosine kinases as new regulators of the mitogenic ERK-dependent pathways in transformed cells. BMC genomics, 15(1), 1169.

Feala JD, et al. (2012) Statistical properties and robustness of biological controller-target networks. PloS one, 7(1), e29374.

Carretero J, et al. (2010) Integrative genomic and proteomic analyses identify targets for Lkb1-deficient metastatic lung tumors. Cancer cell, 17(6), 547.