Resource Summary Report

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NetPhos

RRID:SCR_017975
Type: Tool

Proper Citation

NetPhos (RRID:SCR_017975)

Resource Information

URL: http://www.cbs.dtu.dk/services/NetPhos/

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Description: Web tool as artificial neural network method that predicts phosphorylation sites in independent sequences. Web application based on determination of activity of protein kinases using in vitro assays with either naturally occurring peptides or synthetic peptides. NetPhos 3.1 server predicts serine, threonine or tyrosine phosphorylation sites in eukaryotic proteins using ensembles of neural networks. Both generic and kinase specific predictions are performed. Generic predictions are identical to predictions performed by NetPhos 2.0. Kinase specific predictions are identical to predictions by NetPhosK 1.0. NetPhos 3.1 is available as stand-alone software package.

Synonyms: NetPhos 3.1, NetPhos 2.0

Resource Type: analysis service resource, web service, standalone software, software resource, data access protocol, software application, production service resource, service resource

Defining Citation: PMID:10600390

Keywords: Neural network, predict, phosphorylation site, independent sequence, protein, kinase, serine, threonine, tyrosine, eukaryotic, bio.tools

Availability: Free, Freely available

Resource Name: NetPhos

Resource ID: SCR_017975

Alternate IDs: biotools:netphos

Alternate URLs: https://bio.tools/netphos

Old URLs: http://www.cbs.dtu.dk/services/NetPhos-2.0/

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260805T044419+0000

Ratings and Alerts

No rating or validation information has been found for NetPhos.

No alerts have been found for NetPhos.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 381 mentions in open access literature.

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

Wang P, et al. (2025) NcSWP8, a New Spore Wall Protein, Interacts with Polar Tube Proteins in the Parasitic Microsporidia Vairimorpha (Nosema) ceranae. Microorganisms, 13(1).

He H, et al. (2025) Transcriptome Analysis Reveals the Molecular Mechanism of PLIN1 in Goose Hierarchical and Pre-Hierarchical Follicle Granulosa Cells. Animals : an open access journal from MDPI, 15(2).

Shao D, et al. (2025) The Functional Identification of the CYP2E1 Gene in the Kidney of Lepus yarkandensis. International journal of molecular sciences, 26(2).

Khazaei S, et al. (2025) Designing and Evaluation of a Plasmid Encoding Immunogenic Epitopes From Echinococcus granulosus Eg95-1-6, P29, and GST Against Hydatid Cyst in BALB/c Mice. Journal of parasitology research, 2025, 1655679.

Yang S, et al. (2025) PTPN22-CD45 dual phosphatase retrograde feedback enhances TCR signaling and autoimmunity. Science advances, 11(36), eadw2568.

Yu Y, et al. (2025) Ribosomal protein L27 contributes to virulence and maduramicin resistance in Eimeria tenella. International journal for parasitology. Drugs and drug resistance, 29, 100615.

Li S, et al. (2025) Identification and functional verification of active volatiles recognition by the olfactory co-receptor Orco in Chrysopa pallens (Rambur) (Neuroptera: Chrysopidae). Journal of insect science (Online), 25(4).

Liu F, et al. (2025) AtCHE1, the Arabidopsis homolog of mammalian AATF/Che-1 protein, is involved in safeguarding genome stability. Communications biology, 8(1), 1329.

Hosseini Pouya HS, et al. (2025) Decoding the CBL gene family in durum wheat: Insights into dual ABA signaling pathways and calcium-mediated drought tolerance. The plant genome, 18(3), e70062.

Lu S, et al. (2025) Genome-Wide identification and expression analysis of CsABF/AREB gene family in cucumber (Cucumis sativus L.) and in response to phytohormonal and abiotic stresses. Scientific reports, 15(1), 15757.

Hossen MA, et al. (2025) Computational investigation unveils pathogenic LIG3 non-synonymous mutations and therapeutic targets in acute myeloid leukemia. PloS one, 20(6), e0320550.

Lee YH, et al. (2025) Elucidating the Role and Mechanism of Alpha-Enolase in Senescent Amelioration via Metabolic Reprogramming. Cell proliferation, 58(10), e70049.

Alizadeh Z, et al. (2025) Exploring the influence of symbiosis between arbuscular mycorrhizal fungi and beans on potassium uptake and the activity of AKT and HKT genes. Scientific reports, 15(1), 19169.

Mikitova V, et al. (2025) Complex transcription regulation of acidic chitinase suggests fine-tuning of digestive processes in Drosera binata. Planta, 261(2), 32.

Dong F, et al. (2025) TaSnRK3.23B, a CBL-interacting protein kinase of wheat, confers drought stress tolerance by promoting ROS scavenging in Arabidopsis. BMC plant biology, 25(1), 59.

Bencivenga D, et al. (2025) p27Kip1 and Tumors: Characterization of CDKN1B Variants Identified in MEN4 and Breast Cancer. Cells, 14(3).

Irfan A, et al. (2025) Discovery of bioactive inhibitors targeting onion yellow dwarf virus coat protein based on molecular docking and simulation. BMC plant biology, 25(1), 1720.

Qi M, et al. (2025) Hyperoside, a flavonoid, induces lnc187 and lnc999 to enhance pigeon pea pollen tube growth and seed production. Science advances, 11(46), eadz3499.

Li R, et al. (2025) Phosphoproteomic insights into the regulation of root length in rice (Oryza sativa L. cv. KDML 105): uncovering key events and pathways involving phosphorylated proteins. PeerJ, 13, e19361.

Datta SP, et al. (2025) Evolutionary duplication of the leishmanial adaptor protein ??-SNAP plays a role in its pathogenicity. The Journal of biological chemistry, 301(5), 108427.