Resource Summary Report

Generated by dkNET on May 18, 2025

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

Defining Citation: PMID:10600390

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

Funding:

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: 20250517T060347+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 362 mentions in open access literature.

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

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).

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).

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).

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.

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

Shi Q, et al. (2024) Phospholipase PLCE1 Promotes Transcription and Phosphorylation of MCM7 to Drive Tumor Progression in Esophageal Cancer. Cancer research, 84(4), 560.

Fasawe AS, et al. (2024) KIF3A tail domain phosphorylation is not required for ciliogenesis in mouse embryonic fibroblasts. iScience, 27(3), 109149.

Diep DTV, et al. (2024) A metabolically controlled contact site between vacuoles and lipid droplets in yeast. Developmental cell, 59(6), 740.

Lian C, et al. (2024) Genome-wide identification, characterization and expression pattern analysis of TIFY family members in Artemisia argyi. BMC genomics, 25(1), 925.

Nunes SLP, et al. (2024) Expression of Genes Involved in Banana (Musa spp.) Response to Black Sigatoka. Current issues in molecular biology, 46(12), 13991.

Chen L, et al. (2024) Modeling sporadic juvenile ALS in iPSC-derived motor neurons explores the pathogenesis of FUSR503fs mutation. Frontiers in cellular neuroscience, 18, 1364164.

Zhao J, et al. (2024) Genome-Wide Identification of the ABC Gene Family and Its Expression in Response to the Wood Degradation of Poplar in Trametes gibbosa. Journal of fungi (Basel, Switzerland), 10(2).

Wang T, et al. (2024) Digenic CHD7 and SMCHD1 inheritance Unveils phenotypic variability in a family mainly presenting with hypogonadotropic hypogonadism. Heliyon, 10(1), e23272.

Amjad H, et al. (2024) Comprehensive bioinformatics-based annotation and functional characterization of bovine chymosin protein revealed novel biological insights. Food chemistry. Molecular sciences, 8, 100191.

Panrat T, et al. (2024) Structural modelling and preventive strategy targeting of WSSV hub proteins to combat viral infection in shrimp Penaeus monodon. PloS one, 19(7), e0307976.

Wang B, et al. (2024) Genome-wide analysis of R2R3-MYB transcription factors in poplar and functional validation of PagMYB147 in defense against Melampsora magnusiana. Planta, 260(2), 47.

Zhang J, et al. (2024) Positive Selection of TLR2 and MyD88 Genes Provides Insights Into the Molecular Basis of Immunological Adaptation in Amphibians. Ecology and evolution, 14(12), e70723.

Mu F, et al. (2024) Genome-wide systematic survey and analysis of the RNA helicase gene family and their response to abiotic stress in sweetpotato. BMC plant biology, 24(1), 193.

Sun HY, et al. (2024) PTEN regulated by gga-miR-20a-5p is involved in chicken macrophages inflammatory response to APEC infection via autophagy. Poultry science, 103(11), 104170.

Divya D, et al. (2024) Genome-wide characterization and expression profiling of E2F/DP gene family members in response to abiotic stress in tomato (Solanum lycopersicum L.). BMC plant biology, 24(1), 436.