

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

[iPTMnet](#)

RRID:SCR_014416

Type: Tool

Proper Citation

iPTMnet (RRID:SCR_014416)

Resource Information

URL: <http://research.bioinformatics.udel.edu/iptmnet/>

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Description: A protein database which connects multiple disparate bioinformatics tools and systems text mining, data mining, analysis and visualization tools, and databases and ontologies.

Resource Type: data or information resource, database

Keywords: database, protein, phosphorylation, bioinformatics, text mining, ontology

Funding: NSF ABI-1062520

Availability: Available to the research community

Resource Name: iPTMnet

Resource ID: SCR_014416

License URLs: <http://pir.georgetown.edu/pirwww/about/linkpir.shtml>

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260815T182931+0000

Ratings and Alerts

No rating or validation information has been found for iPTMnet.

No alerts have been found for iPTMnet.

Data and Source Information

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Lai X, et al. (2026) CLDN7: Epithelial gatekeeper from physiology to pathology?roles in cancer and epithelial?related diseases (Review). International journal of molecular medicine, 57(5).

Anandakrishnan M, et al. (2025) KSMoFinder - Knowledge graph embedding of proteins and motifs for predicting kinases of human phosphosites. bioRxiv : the preprint server for biology.

Zhao MX, et al. (2025) Decoding protein N-phosphorylation functionality and sequence patterns. Briefings in bioinformatics, 26(6).

Koul S, et al. (2025) Mapping the Subtype-Specific PARP1 ADP-ribosylated Proteome in Breast Cancer Cells. bioRxiv : the preprint server for biology.

Zhao MX, et al. (2024) Nphos: Database and Predictor of Protein N-phosphorylation. Genomics, proteomics & bioinformatics, 22(3).

Nezamuldeen L, et al. (2024) Boolean Modeling of Biological Network Applied to Protein-Protein Interaction Network of Autism Patients. Biology, 13(8).

Mianesaz H, et al. (2024) Genetic variant profiling of neonatal diabetes mellitus in Iranian patients: Unveiling 58 distinct variants in 14 genes. Journal of diabetes investigation, 15(10), 1390.

Zhou Y, et al. (2024) Pan-cancer analysis of Sp1 with a focus on immunomodulatory roles in gastric cancer. Cancer cell international, 24(1), 338.

Sekar JAP, et al. (2024) A web portal for exploring kinase-substrate interactions. NPJ systems biology and applications, 10(1), 113.

Zhao W, et al. (2023) Unravel the regulatory mechanism of Yrr1p phosphorylation in response to vanillin stress in Saccharomyces cerevisiae. Microbial cell factories, 22(1), 48.

Mianesaz H, et al. (2023) Causative variants linked with limb girdle muscular dystrophy in an Iranian population: 6 novel variants. Molecular genetics & genomic medicine, 11(2), e2101.

Abbaali I, et al. (2023) The tubulin database: Linking mutations, modifications, ligands and local interactions. PloS one, 18(12), e0295279.

Gavali S, et al. (2022) A knowledge graph representation learning approach to predict novel kinase-substrate interactions. Molecular omics, 18(9), 853.

Tasleem M, et al. (2021) Investigation of Antidepressant Properties of Yohimbine by Employing Structure-Based Computational Assessments. *Current issues in molecular biology*, 43(3), 1805.

Rosales M, et al. (2021) Phosphoproteomic Landscape of AML Cells Treated with the ATP-Competitive CK2 Inhibitor CX-4945. *Cells*, 10(2).

Zou G, et al. (2021) Development of an experiment-split method for benchmarking the generalization of a PTM site predictor: Lysine methylome as an example. *PLoS computational biology*, 17(12), e1009682.

Ali A, et al. (2021) Clinical, Biochemical, and Genetic Heterogeneity in Glutaric Aciduria Type II Patients. *Genes*, 12(9).

Attri S, et al. (2021) Dissecting role of founder mutation p.V727M in GNE in Indian HIBM cohort. *Open medicine (Warsaw, Poland)*, 16(1), 1733.

Wang H, et al. (2021) The Distinct Properties of the Consecutive Disordered Regions Inside or Outside Protein Domains and Their Functional Significance. *International journal of molecular sciences*, 22(19).

Sakaya GR, et al. (2021) Peptidomic profiling of cerebrospinal fluid from patients with intracranial saccular aneurysms. *Journal of proteomics*, 240, 104188.