

# Resource Summary Report

Generated by [NIF](#) on Sep 15, 2026

## [iPTMnet](#)

RRID:SCR\_014416

Type: Tool

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### Proper Citation

iPTMnet (RRID:SCR\_014416)

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### Resource Information

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

**Proper Citation:** iPTMnet (RRID:SCR\_014416)

**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:** 20260912T200214+0000

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### Ratings and Alerts

No rating or validation information has been found for iPTMnet.

No alerts have been found for iPTMnet.

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### 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 [NIF](#) .

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.