

Resource Summary Report

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dbPTM: An informational repository of proteins and post-translational modifications

RRID:SCR_007619

Type: Tool

Proper Citation

dbPTM: An informational repository of proteins and post-translational modifications
(RRID:SCR_007619)

Resource Information

URL: <http://dbptm.mbc.nctu.edu.tw/>

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Description: dbPTM is a database that compiles information on protein post-translational modifications (PTM) such as the modified sites, solvent accessibility of surrounding amino acids, protein secondary and tertiary structures, protein domains, and protein variations. The version 2.0 of dbPTM integrates the experimentally validated PTM sites with referable literatures from Swiss-Prot, Phospho.ELM, O-GLYCBASE, and UbiProt. In all of the collected PTM information, about 25 types of PTM with enough experimentally validated sites are trained the profile hidden Markov models (HMMs) to detect the potential PTM sites with 100% specificity against Swiss-Prot proteins. To help users investigating more detail in each type of PTM, the substrate peptide specificity such as positional amino acid frequency, solvent accessibility and secondary structure surrounding the modified sites are also provided. Moreover, the information of orthologous protein clusters is provided to users for analyzing whether the PTM sites located in the evolutionary conserved regions or not., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: dbPTM

Resource Type: database, data or information resource

Keywords: protein, protein post-translational modification, ptm

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: dbPTM: An informational repository of proteins and post-translational modifications

Resource ID: SCR_007619

Alternate IDs: nif-0000-02730

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260805T044156+0000

Ratings and Alerts

No rating or validation information has been found for dbPTM: An informational repository of proteins and post-translational modifications.

No alerts have been found for dbPTM: An informational repository of proteins and post-translational modifications.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 112 mentions in open access literature.

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

Leban T, et al. (2026) Multiomics Data Synthesis of FAM83H in Amelogenesis Imperfecta. International dental journal, 76(1), 109293.

Medvedev KE, et al. (2025) Leveraging AI to Explore Structural Contexts of Post-Translational Modifications in Drug Binding. bioRxiv : the preprint server for biology.

Li SJ, et al. (2025) LIMK1 as a Novel Kinase of β -Catenin Promotes Esophageal Cancer Metastasis by Cooperating With CDK5. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(29), e03223.

Peng FZ, et al. (2025) PTM-Mamba: a PTM-aware protein language model with bidirectional gated Mamba blocks. Nature methods, 22(5), 945.

Arroyo Villora S, et al. (2025) Epigenetic silencing and CRISPR-mediated reactivation of tight junction protein claudin10b (CLDN10B) in renal cancer. Clinical epigenetics, 17(1), 102.

Gao Y, et al. (2025) Pan-cancer analysis reveals netrin-1 receptors as potential tumor biomarkers and immune-related therapeutic targets. Scientific reports, 15(1), 44015.

Zafar A, et al. (2025) Molecular dynamics simulations of intrinsically disordered protein regions enable biophysical interpretation of variant effect predictors. bioRxiv : the preprint server for biology.

Medvedev KE, et al. (2025) Leveraging AI to explore structural contexts of post-translational modifications in drug binding. *Journal of cheminformatics*, 17(1), 67.

Zhu L, et al. (2025) RLSuccSite: succinylation sites prediction based on reinforcement learning dynamic with balanced reward mechanism and three-peaks enhanced method for physicochemical property scores. *Journal of cheminformatics*, 17(1), 92.

Ibrahim IH, et al. (2025) Altered protein lipidation in cancer: A hidden link to sensory neuronal dysfunction. *Computational biology and chemistry*, 120(Pt 1), 108656.

Cho D, et al. (2024) Autoinhibited Protein Database: a curated database of autoinhibitory domains and their autoinhibition mechanisms. *Database : the journal of biological databases and curation*, 2024.

Prieto G, et al. (2024) Enhancing prediction of short linear protein motifs with Wregex 3.0. *Computational and structural biotechnology journal*, 23, 2978.

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Gou Y, et al. (2024) GPS-SUMO 2.0: an updated online service for the prediction of SUMOylation sites and SUMO-interacting motifs. *Nucleic acids research*, 52(W1), W238.

Pakhrin SC, et al. (2024) Prediction of human O-linked glycosylation sites using stacked generalization and embeddings from pre-trained protein language model. *Bioinformatics (Oxford, England)*, 40(11).

Zhang L, et al. (2024) DeepO-GlcNAc: a web server for prediction of protein O-GlcNAcylation sites using deep learning combined with attention mechanism. *Frontiers in cell and developmental biology*, 12, 1456728.

Palacios AV, et al. (2024) SumoPred-PLM: human SUMOylation and SUMO2/3 sites Prediction using Pre-trained Protein Language Model. *NAR genomics and bioinformatics*, 6(1), lqae011.

Ertelt M, et al. (2024) Combining machine learning with structure-based protein design to predict and engineer post-translational modifications of proteins. *PLoS computational biology*, 20(3), e1011939.

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

Deutsch N, et al. (2023) DisCanVis: Visualizing integrated structural and functional annotations to better understand the effect of cancer mutations located within disordered proteins. *Protein science : a publication of the Protein Society*, 32(1), e4522.