

Resource Summary Report

Generated by T1D on Jul 28, 2026

PTMcode

RRID:SCR_002046

Type: Tool

Proper Citation

PTMcode (RRID:SCR_002046)

Resource Information

URL: <http://ptmcode.embl.de/>

Proper Citation: PTMcode (RRID:SCR_002046)

Description: Database of known and predicted functional associations between protein posttranslational modifications (PTMs) within proteins. In its first release it contains 13 different PTM types. PTM types are abbreviated in a two letter code as: Ph (phosphorylation), NG (N-linked glycosylation), Ac (acetylation), OG (O-linked glycosylation), Ub (ubiquitination), Me (methylation), SM (SUMOylation), Hy (hydroxylation), Ca (carboxylation), Pa (palmitoylation), Su (sulfation), Ni (nitrosylation) and CG (C-linked glycosylation). These PTMs are present in 25,765 proteins of 8 different eukaryotes. The database is focused on the exploration of the global post-translational regulation of proteins, not only by describing the set of its modifications, but by identifying the functional associations among the PTMs present in the protein. To do that, they combine five different evidence channels based on a literature survey, the modified residue co-evolution, their structural proximity, their competition for the same residue and the location within PTM highly-enriched protein regions (hotspots) and show the functional associations within the context of the protein architecture.

Abbreviations: PTMCode

Resource Type: database, data or information resource

Defining Citation: [PMID:23193284](#)

Keywords: protein posttranslational modification, protein, function, phosphorylation, n-linked glycosylation, acetylation, o-linked glycosylation, ubiquitination, methylation, sumoylation, hydroxylation, carboxylation, palmitoylation, sulfation, nitrosylation, c-linked glycosylation

Availability: Free, Freely available

Resource Name: PTMcode

Resource ID: SCR_002046

Alternate IDs: OMICS_01915

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Record Creation Time: 20220129T080211+0000

Record Last Update: 20260725T191121+0000

Ratings and Alerts

No rating or validation information has been found for PTMcode.

No alerts have been found for PTMcode.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Esmaili F, et al. (2023) A Review of Machine Learning and Algorithmic Methods for Protein Phosphorylation Site Prediction. Genomics, proteomics & bioinformatics, 21(6), 1266.

Abid F, et al. (2023) Non-synonymous SNPs variants of PRKCG and its association with oncogenes predispose to hepatocellular carcinoma. Cancer cell international, 23(1), 123.

Wu X, et al. (2023) Targeting protein modifications in metabolic diseases: molecular mechanisms and targeted therapies. Signal transduction and targeted therapy, 8(1), 220.

Leutert M, et al. (2021) Decoding Post-Translational Modification Crosstalk With Proteomics. Molecular & cellular proteomics : MCP, 20, 100129.

Li W, et al. (2021) Insights into the post-translational modification and its emerging role in shaping the tumor microenvironment. Signal transduction and targeted therapy, 6(1), 422.

Smythers AL, et al. (2021) Mapping the plant proteome: tools for surveying coordinating pathways. Emerging topics in life sciences, 5(2), 203.

Y??Imaz S, et al. (2021) Robust inference of kinase activity using functional networks. Nature communications, 12(1), 1177.

He D, et al. (2020) Advances on Plant Ubiquitylome-From Mechanism to Application. International journal of molecular sciences, 21(21).

Muggia L, et al. (2020) An Overview of Genomics, Phylogenomics and Proteomics Approaches in Ascomycota. *Life* (Basel, Switzerland), 10(12).

Li Y, et al. (2017) Co-occurring protein phosphorylation are functionally associated. *PLoS computational biology*, 13(5), e1005502.

Sun B, et al. (2015) Nonsynonymous Single-Nucleotide Variations on Some Posttranslational Modifications of Human Proteins and the Association with Diseases. *Computational and mathematical methods in medicine*, 2015, 124630.

Minguez P, et al. (2015) PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. *Nucleic acids research*, 43(Database issue), D494.

Duan G, et al. (2015) The roles of post-translational modifications in the context of protein interaction networks. *PLoS computational biology*, 11(2), e1004049.