

Resource Summary Report

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PhosphoSitePlus: Protein Modification Site

RRID:SCR_001837

Type: Tool

Proper Citation

PhosphoSitePlus: Protein Modification Site (RRID:SCR_001837)

Resource Information

URL: <http://www.phosphosite.org>

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Description: A freely accessible on-line systems biology resource devoted to all aspects of protein modification, as well as other post-translational modifications. It provides valuable and unique tools for both cell biologists and mass spectroscopists. PhosphoSite is a human- and mouse-centric database. It includes features such as: viewing the locations of modified residues on molecular models; browsing and searching MS2 records by disease, tissue, and cell line; submitting lists of peptides to identify previously reported genes; searching by sub-cellular localization, treatment, tissues, cell types, cell lines and diseases, and protein types and protein domains; searching for experimentally-verified kinase substrates and viewing preferred substrate motifs; and viewing MS2 spectra for peptides and sites not previously published.

Abbreviations: PSP

Synonyms: PhosphoSitePlus, PhosphoSite

Resource Type: data or information resource, knowledge environment resource, portal

Defining Citation: [PMID:22135298](#)

Keywords: portal, mass spectroscopist, molecular model, mouse, post translational, subcellular localization, protein modification, post-translational modification, protein phosphorylation, protein structure, protein function, ubiquitinylation, acetylation, cellular component, cell type, visualization, data repository, bio.tools, FASEB list

Funding: NCI ;
NIAAA R44 AA014848;
NIGMS R43 GM65768

Availability: Free, Freely available

Resource Name: PhosphoSitePlus: Protein Modification Site

Resource ID: SCR_001837

Alternate IDs: biotools:phosphositeplus, nif-0000-10399

Alternate URLs: <https://bio.tools/phosphositeplus>

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Record Creation Time: 20220129T080209+0000

Record Last Update: 20260912T195532+0000

Ratings and Alerts

No rating or validation information has been found for PhosphoSitePlus: Protein Modification Site.

No alerts have been found for PhosphoSitePlus: Protein Modification Site.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1003 mentions in open access literature.

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

Hu ZK, et al. (2026) HDAC6-mediated PFKL deacetylation enhances aerobic glycolysis and promotes VSMC proliferation. The Journal of biological chemistry, 302(2), 111075.

Yang WS, et al. (2026) Phosphorylation at S1288 of leukemia associated RhoGEF (LARG/ARHGEF12) induces plasma membrane localization and promotes binding and activation of RhoA. The Journal of biological chemistry, 302(1), 110996.

Lin CP, et al. (2026) The Mechanism of Histone Ubiquitylation by the ASB9-CUL5 Ubiquitin Ligase. Molecular & cellular proteomics : MCP, 25(2), 101471.

Cho Y, et al. (2026) KDM4A Erases the H3R17me2a Mark, Facilitating Chromosome Condensation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(26), e14281.

Sawaya BE, et al. (2026) CK1?-dependent SNAPIN dysregulation drives lysosomal failure in HIV-1 Vpr-exposed neurons: A targetable mechanism in HAND. iScience, 29(2), 114544.

Zhang J, et al. (2026) OTUD1 delays wound healing by regulating endothelial function and angiogenesis in diabetic mice. Journal of advanced research, 80, 1063.

- Wetterwald L, et al. (2026) MYCT1-IFITM2/3 interaction links endothelial endolysosomal trafficking to white adipose tissue expansion. *The Journal of experimental medicine*, 223(5).
- Serafino G, et al. (2026) Mechanical Cues Regulate Cargo Sorting and Export at the Golgi. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e06241.
- de la Iglesia A, et al. (2026) Multiple Roles of Protamine Kinase SRPK1 and Phosphatase PP1? in Sperm Development. *Proteomics*, 26(7), 42.
- Mayer MP, et al. (2026) Wiring of cellular proteostasis by J-domain proteins. *Cell stress & chaperones*, 31(4), 100191.
- Haile B, et al. (2026) MOKCa-3D database: functional and structural analysis of missense mutations in cancer. *Database : the journal of biological databases and curation*, 2026.
- Begum S, et al. (2026) In Silico Phosphoproteomic Analysis Reveals Divergent Regulation of Presenilin 1 and Presenilin 2. *Neuromolecular medicine*, 28(1), 5.
- Qian P, et al. (2026) Time-of-day effects on post-exercise phosphoproteomic profiling in mouse hippocampus. *Frontiers in cell and developmental biology*, 14, 1788597.
- Chen S, et al. (2026) Hypoxia-induced PRMT6 expression promotes temozolomide chemoresistance in glioblastoma via G3BP1. *Journal of translational medicine*, 24(1), 226.
- Sain R, et al. (2026) Genetic and genomic approaches to explore roles for the conserved 3'-5' exoribonuclease EXOSC10 in normal and malignant cells. *RNA (New York, N.Y.)*, 32(6), 789.
- Du A, et al. (2026) DCLK1 drives malignant progression and chemoresistance of bladder cancer by deubiquitinating HDAC6. *Molecular cancer*, 25(1).
- Heller EM, et al. (2026) Protein buffering of aneuploidy is driven by coordinated factors identified through machine learning. *Molecular systems biology*, 22(4), 563.
- Wen S, et al. (2026) EIF4B Ser93 phosphorylation by ERK2 promotes epithelial-mesenchymal transition to drive colorectal cancer metastasis. *Cell death & disease*, 17(1), 178.
- Kohoutova K, et al. (2026) Structural basis of the cyclin Y/14-3-3 protein-mediated activation of CDK16. *Nature communications*, 17(1).
- Ma F, et al. (2026) Proteome profiles of esophageal squamous cell carcinoma tie mitochondrial complex I to immunotherapy. *EMBO molecular medicine*, 18(5), 1884.