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: knowledge environment resource, data or information 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: 20260729T044026+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 903 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Serafino G, et al. (2026) Mechanical Cues Regulate Cargo Sorting and Export at the Golgi. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(1), e06241.

Cai Z, et al. (2026) The Cullin3-Ring E3 ubiquitin ligase complex and USP14 regulate spastin-mediated microtubule severing and promotion of neurite outgrowth. Neural regeneration research, 21(4), 1641.

Wang W, et al. (2026) Feedback regulation between histone H3 lysine 18 lactylation and TROP2-mediated glycolysis drives metastatic progression of colorectal cancer. Clinical and translational medicine, 16(1), e70562.

Stastna M, et al. (2025) Post-translational modifications of proteins in cardiovascular diseases examined by proteomic approaches. The FEBS journal, 292(1), 28.

Romero JC, et al. (2025) Loss of CD98HC phosphorylation by ATM impairs antiporter trafficking and drives glutamate toxicity in Ataxia telangiectasia. Nature communications, 16(1), 5109.

Park IY, et al. (2025) A novel cardiomyopathy phenotype linked to a CHD7 missense variant. Scientific reports, 15(1), 19429.

Fu Y, et al. (2025) Integrative Multi-Omics Approaches Reveal Selectivity Profiles and Molecular Mechanisms of FIIN-2, a Covalent FGFR Inhibitor. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(14), e2412578.

Abellan S, et al. (2025) Impact of Gemin5 in protein synthesis: phosphoresidues of the dimerization domain regulate ribosome binding. RNA biology, 22(1), 1.

Miao Y, et al. (2025) Histone Acetyltransferase MOF-Mediated AURKB K215 Acetylation Drives Breast Cancer Cell Proliferation via c-MYC Stabilization. Cells, 14(14).

Planells-Cases R, et al. (2025) Endosomal chloride/proton exchangers need inhibitory TMEM9 ??-subunits for regulation and prevention of disease-causing overactivity. Nature communications, 16(1), 3117.

Chen H, et al. (2025) The SIK3-N783Y mutation is associated with the human natural short sleep trait. Proceedings of the National Academy of Sciences of the United States of America, 122(19), e2500356122.

Huang YY, et al. (2025) EGFR phosphorylates DNAJB1 to suppress ??-synuclein aggregation in Parkinson's disease. NPJ Parkinson's disease, 11(1), 157.

Ma Y, et al. (2025) The Nuclear Localization of ACLY Guards Early Embryo Development Through Recruiting P300 and HAT1 to Promote Histone Acetylation and Transcription. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(31), e14367.

Shao N, et al. (2025) USP5 stabilizes YTHDF1 to control cancer immune surveillance through mTORC1-mediated phosphorylation. Nature communications, 16(1), 1313.

Segura-Roman A, et al. (2025) Autophagosomes anchor an AKAP11-dependent regulatory checkpoint that shapes neuronal PKA signaling. The EMBO journal, 44(11), 3150.

Xu S, et al. (2025) Bending the boundaries: the many facets of endophilin-As from membrane dynamics to disease. Cellular and molecular life sciences : CMLS, 82(1), 339.

Basilone NT, et al. (2025) Canonical and alternate mechanisms that regulate ubiquitylation by the E3 ligase parkin. Biochemical Society transactions, 53(4), 1053.

Sharma N, et al. (2025) Phosphoregulation of RAD51AP1 function in homology-directed repair. bioRxiv : the preprint server for biology.

Koit S, et al. (2025) A conserved phosphorylation mechanism for regulating the interaction between the CMG replicative helicase and its forked DNA substrate. The Journal of biological chemistry, 301(4), 108408.

Zhou Y, et al. (2025) Clinical and functional significance of SPATA2 in cancer particularly in LIHC. Scientific reports, 15(1), 8392.