

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

Phospho.ELM

RRID:SCR_001109

Type: Tool

Proper Citation

Phospho.ELM (RRID:SCR_001109)

Resource Information

URL: <http://phospho.elm.eu.org/>

Proper Citation: Phospho.ELM (RRID:SCR_001109)

Description: Database of experimentally verified phosphorylation sites in eukaryotic proteins. Entries are manually curated with links to literature references, information about structure, interaction partners and sub-cellular compartment tissues, and sequences from the UniProt database.

Resource Type: database, data or information resource

Defining Citation: [PMID:17962309](#)

Keywords: eukaryotic protein, phosphorylation site, database, curation, bio.tools, FASEB list

Availability: Publicly available

Resource Name: Phospho.ELM

Resource ID: SCR_001109

Alternate IDs: nif-0000-03278, biotools:phosphoelm

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

License: Academic Software License

License URLs: <http://phospho.elm.eu.org/disclaimer.html>

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260725T191118+0000

Ratings and Alerts

No rating or validation information has been found for Phospho.ELM.

No alerts have been found for Phospho.ELM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Vilardell J, et al. (2018) The importance of negative determinants as modulators of CK2 targeting. The lesson of Akt2 S131. PloS one, 13(3), e0193479.

Yángüez E, et al. (2018) Phosphoproteomic-based kinase profiling early in influenza virus infection identifies GRK2 as antiviral drug target. Nature communications, 9(1), 3679.

Xu H, et al. (2017) Mass spectrometry-based quantification of the cellular response to ultraviolet radiation in HeLa cells. PloS one, 12(11), e0186806.

Qiao Z, et al. (2017) Proteomic approach toward determining the molecular background of pazopanib resistance in synovial sarcoma. Oncotarget, 8(65), 109587.

Oyama R, et al. (2017) Generation of novel patient-derived CIC- DUX4 sarcoma xenografts and cell lines. Scientific reports, 7(1), 4712.

Richter E, et al. (2016) Proteomic discovery of host kinase signaling in bacterial infections. Proteomics. Clinical applications, 10(9-10), 994.

Giniatullina A, et al. (2015) Functional characterization of the PCLO p.Ser4814Ala variant associated with major depressive disorder reveals cellular but not behavioral differences. Neuroscience, 300, 518.

Çelen ?, et al. (2015) Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PloS one, 10(10), e0141773.

Chen T, et al. (2015) Web resources for mass spectrometry-based proteomics. Genomics, proteomics & bioinformatics, 13(1), 36.

López Villar E, et al. (2015) Study of phosphorylation events for cancer diagnoses and treatment. Clinical and translational medicine, 4(1), 59.

Stathopoulou K, et al. (2014) Four-and-a-half LIM domains proteins are novel regulators of the protein kinase D pathway in cardiac myocytes. The Biochemical journal, 457(3), 451.

Wu X, et al. (2014) Activation of diverse signalling pathways by oncogenic PIK3CA mutations. Nature communications, 5, 4961.

Datta S, et al. (2014) An ensemble method approach to investigate kinase-specific phosphorylation sites. *International journal of nanomedicine*, 9, 2225.

Jahangir Z, et al. (2014) Alternate Phosphorylation/O-GlcNAc Modification on Human Insulin IRSs: A Road towards Impaired Insulin Signaling in Alzheimer and Diabetes. *Advances in bioinformatics*, 2014, 324753.

Fujita S, et al. (2013) An atypical tubulin kinase mediates stress-induced microtubule depolymerization in Arabidopsis. *Current biology : CB*, 23(20), 1969.

Halcsik E, et al. (2013) New insights in osteogenic differentiation revealed by mass spectrometric assessment of phosphorylated substrates in murine skin mesenchymal cells. *BMC cell biology*, 14, 47.

Patrick R, et al. (2012) Mapping the stabilome: a novel computational method for classifying metabolic protein stability. *BMC systems biology*, 6, 60.

Garaguso I, et al. (2012) A rapid screening assay to search for phosphorylated proteins in tissue extracts. *PloS one*, 7(11), e50025.

Peppelenbosch MP, et al. (2012) Kinome profiling. *Scientifica*, 2012, 306798.

Bergström Lind S, et al. (2011) Toward a comprehensive characterization of the phosphotyrosine proteome. *Cellular signalling*, 23(8), 1387.