

# Resource Summary Report

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## PhosPhAt

RRID:SCR\_003332

Type: Tool

### Proper Citation

PhosPhAt (RRID:SCR\_003332)

### Resource Information

**URL:** <http://phosphat.uni-hohenheim.de/>

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**Description:** Database containing information on Arabidopsis phosphorylation sites which were identified by mass spectrometry in large scale experiments from different research groups. Specific information on the peptide properties as well as on the experimental and analytical context is given. The PhosPhAt service has a built-in plant specific phosphorylation site predictor trained on the experimental dataset for Serine, threonine and tyrosine phosphorylation (pSer, pThr, pTyr). Protein sequences or Arabidopsis AGI gene identifier can be submitted to the predictor. Users and researchers are encouraged to assist in keeping the database current by submitting either published data or unpublished data (MS/MS data required).

**Abbreviations:** PhosPhAt

**Synonyms:** Arabidopsis Protein Phosphorylation Site Database

**Resource Type:** analysis service resource, data analysis service, data or information resource, data repository, database, production service resource, service resource, storage service resource

**Defining Citation:** [PMID:23172287](#), [PMID:19880383](#), [PMID:17984086](#)

**Keywords:** phosphorylation, peptide, function, mass spectrometry, kinase, serine, threonine, tyrosine, phosphoprotein, phosphopeptide, tryptic phosphopeptide, serine phosphosite, threonine phosphosite, tyrosine phosphosite, FASEB list

**Availability:** Free, Freely available

**Resource Name:** PhosPhAt

**Resource ID:** SCR\_003332

**Alternate IDs:** nif-0000-03277

**Old URLs:** <http://phosphat.mpimp-golm.mpg.de/app.html>

**Record Creation Time:** 20220129T080218+0000

**Record Last Update:** 20260829T182152+0000

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## Ratings and Alerts

No rating or validation information has been found for PhosPhAt.

No alerts have been found for PhosPhAt.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 62 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Takase H, et al. (2026) Dynamic and Basal Phosphorylation Landscapes of Absciscic Acid Signaling Revealed by Phosphoproteome Analysis in Arabidopsis. International journal of molecular sciences, 27(8).

Gitman IFB, et al. (2026) OmicIntegrator: A Simple and Versatile Tool for Meta-Analysis. Plants (Basel, Switzerland), 15(2).

Cho Y, et al. (2026) Fully Tunable Phosphorylation of RPS6A Ensures the Successful Development of Arabidopsis Seedlings. Plant, cell & environment, 49(5), 2783.

Fang Y, et al. (2025) Calcium signaling-mediated phosphorylation controls zinc allocation in Arabidopsis. Stress biology, 5(1), 78.

Linnenbrügger L, et al. (2025) Evidence for peroxisomal redundancy among the glucose-6-phosphate dehydrogenase isoforms of Arabidopsis thaliana. Plant & cell physiology, 66(5), 722.

Matthes MS, et al. (2025) Distinct domains of ENHANCER OF PINOID hold information for its polarization required for auxin-mediated cotyledon and flower development in Arabidopsis. PLoS genetics, 21(6), e1011217.

Domingo G, et al. (2024) The cAMP-dependent phosphorylation footprint in response to heat stress. Plant cell reports, 43(6), 137.

Henning PM, et al. (2024) Phosphoproteomic analysis of distylous Turnera subulata identifies pathways related to endoreduplication that correlate with reciprocal herkogamy.

American journal of botany, 111(12), e16438.

Jorge GL, et al. (2024) Unveiling orphan receptor-like kinases in plants: novel client discovery using high-confidence library predictions in the Kinase-Client (KiC) assay. *Frontiers in plant science*, 15, 1372361.

Ahsan N, et al. (2024) Decoding *Arabidopsis thaliana* CPK/SnRK Superfamily Kinase Client Signaling Networks Using Peptide Library and Mass Spectrometry. *Plants (Basel, Switzerland)*, 13(11).

Doering LN, et al. (2024) Evidence for dual targeting control of *Arabidopsis* 6-phosphogluconate dehydrogenase isoforms by N-terminal phosphorylation. *Journal of experimental botany*, 75(10), 2848.

Jain D, et al. (2024) Protein Phosphorylation Orchestrates Acclimations of *Arabidopsis* Plants to Environmental pH. *Molecular & cellular proteomics : MCP*, 23(1), 100685.

Colin L, et al. (2023) The cell biology of primary cell walls during salt stress. *The Plant cell*, 35(1), 201.

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

Elshobaky A, et al. (2023) Protein-Protein Interactions and Quantitative Phosphoproteomic Analysis Reveal Potential Mitochondrial Substrates of Protein Phosphatase 2A-B'? Holoenzyme. *Plants (Basel, Switzerland)*, 12(13).

Romero-Hernandez G, et al. (2022) Plant Kinases in the Perception and Signaling Networks Associated With Arthropod Herbivory. *Frontiers in plant science*, 13, 824422.

Zhang C, et al. (2022) ROPGAP-dependent interaction between brassinosteroid and ROP2-GTPase signaling controls pavement cell shape in *Arabidopsis*. *Current biology : CB*, 32(3), 518.

Romeiro Motta M, et al. (2022) B1-type cyclins control microtubule organization during cell division in *Arabidopsis*. *EMBO reports*, 23(1), e53995.

Li Q, et al. (2022) Quantitative phosphoproteomics reveals the role of wild soybean GsSnRK1 as a metabolic regulator under drought and alkali stresses. *Journal of proteomics*, 258, 104528.

Vogel K, et al. (2022) Lipid-mediated activation of plasma membrane-localized deubiquitylating enzymes modulate endosomal trafficking. *Nature communications*, 13(1), 6897.