Resource Summary Report

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Plant Protein Phosphorylation Database

RRID:SCR_007841
Type: Tool

Proper Citation

Plant Protein Phosphorylation Database (RRID:SCR_007841)

Resource Information

URL: http://www.p3db.org

Proper Citation: Plant Protein Phosphorylation Database (RRID:SCR_007841)

Description: It was established with an overall objective to provide a resource of protein phosphorylation data from multiple plants. P3DB was constructed with a dataset from oilseed rape. The data was obtained using a combination of data-dependent neutral loss and multistage activation mass spectrometry. The dataset includes 14,670 non-redundant phosphorylation sites from 8,894 phospho-peptides in 6,382 substrate proteins.

Abbreviations: P3DB

Synonyms: Plant Protein Phosphorylation Database

Resource Type: database, data or information resource

Keywords: FASEB list

Funding:

Resource Name: Plant Protein Phosphorylation Database

Resource ID: SCR_007841

Alternate IDs: nif-0000-03235

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250412T055216+0000

Ratings and Alerts

No rating or validation information has been found for Plant Protein Phosphorylation Database.

No alerts have been found for Plant Protein Phosphorylation Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Koh E, et al. (2024) Confronting the data deluge: How artificial intelligence can be used in the study of plant stress. Computational and structural biotechnology journal, 23, 3454.

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

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

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

Zhang Q, et al. (2020) Genome- and Transcriptome-Wide Identification of C3Hs in Common Bean (Phaseolus vulgaris L.) and Structural and Expression-Based Analyses of Their Functions During the Sprout Stage Under Salt-Stress Conditions. Frontiers in genetics, 11, 564607.

Gao ZF, et al. (2020) Large-scale Proteomic and Phosphoproteomic Analyses of Maize Seedling Leaves During De-etiolation. Genomics, proteomics & bioinformatics, 18(4), 397.

Zhao M, et al. (2020) Genome-Wide Identification of the TCP Gene Family in Broussonetia papyrifera and Functional Analysis of BpTCP8, 14 and 19 in Shoot Branching. Plants (Basel, Switzerland), 9(10).

Lu J, et al. (2020) Global Quantitative Proteomics Studies Revealed Tissue-Preferential Expression and Phosphorylation of Regulatory Proteins in Arabidopsis. International journal of molecular sciences, 21(17).

Li Y, et al. (2019) Genome-wide identification, characterisation and functional evaluation of WRKY genes in the sweet potato wild ancestor Ipomoea trifida (H.B.K.) G. Don. under

abiotic stresses. BMC genetics, 20(1), 90.

Yang Z, et al. (2019) Genome-wide identification, structural and gene expression analysis of the bZIP transcription factor family in sweet potato wild relative Ipomoea trifida. BMC genetics, 20(1), 41.

Baek D, et al. (2019) AtPR5K2, a PR5-Like Receptor Kinase, Modulates Plant Responses to Drought Stress by Phosphorylating Protein Phosphatase 2Cs. Frontiers in plant science, 10, 1146.

Song Q, et al. (2019) Identification and Analysis of Micro-Exon Genes in the Rice Genome. International journal of molecular sciences, 20(11).

Arsova B, et al. (2018) Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. Frontiers in plant science, 9, 1168.

Liebthal M, et al. (2018) Peroxiredoxins and Redox Signaling in Plants. Antioxidants & redox signaling, 28(7), 609.

Ahsan N, et al. (2017) Comparative proteomic analysis provides insight into the biological role of protein phosphatase inhibitor-2 from Arabidopsis. Journal of proteomics, 165, 51.

Mattei B, et al. (2016) Comprehensive Analysis of the Membrane Phosphoproteome Regulated by Oligogalacturonides in Arabidopsis thaliana. Frontiers in plant science, 7, 1107.

Rattanakan S, et al. (2016) Relative quantification of phosphoproteomic changes in grapevine (Vitis vinifera L.) leaves in response to abscisic acid. Horticulture research, 3, 16029.

Romero-Rodríguez MC, et al. (2015) Multiplex staining of 2-DE gels for an initial phosphoproteome analysis of germinating seeds and early grown seedlings from a non-orthodox specie: Quercus ilex L. subsp. ballota [Desf.] Samp. Frontiers in plant science, 6, 620.

Hou Y, et al. (2015) A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. BMC plant biology, 15, 163.

Aryal UK, et al. (2015) Enrichment and Analysis of Intact Phosphoproteins in Arabidopsis Seedlings. PloS one, 10(7), e0130763.