

Resource Summary Report

Generated by [T1D](#) on Sep 16, 2026

Musite

RRID:SCR_012141

Type: Tool

Proper Citation

Musite (RRID:SCR_012141)

Resource Information

URL: <http://musite.sourceforge.net/>

Proper Citation: Musite (RRID:SCR_012141)

Description: A Java-based standalone application for predicting both general and kinase-specific protein phosphorylation sites.

Resource Type: software resource

Defining Citation: [PMID:20702892](#)

Keywords: standalone software, java

Resource Name: Musite

Resource ID: SCR_012141

Alternate IDs: OMICS_05941

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260912T195746+0000

Ratings and Alerts

No rating or validation information has been found for Musite.

No alerts have been found for Musite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Lynch TJ, et al. (2026) ABI5-binding proteins are substrates of key components in the ABA core signaling pathway affecting seeds. *Plant physiology*, 200(1).

Khaskhali S, et al. (2025) Expression profile and characterization of respiratory burst oxidase homolog genes in rice under MeJA, SA and Xoo treatments. *Scientific reports*, 15(1), 5936.

Baek W, et al. (2025) Phosphorylation-Induced Degradation of Pepper Dehydration-Related Homeobox Gene 12 (CaDRHB12), a Negative Regulator of Drought Response in Pepper, by CaSnRK2.6 Enhances Drought Tolerance. *Plant biotechnology journal*, 23(11), 5178.

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.

Diwan D, et al. (2021) A Quantitative Arabidopsis IRE1a Ribonuclease-Dependent in vitro mRNA Cleavage Assay for Functional Studies of Substrate Splicing and Decay Activities. *Frontiers in plant science*, 12, 707378.

Liu W, et al. (2020) Genome-wide characterization and expression analysis of soybean trihelix gene family. *PeerJ*, 8, e8753.

Devi SJSR, et al. (2020) Identification and Characterization of a Large Effect QTL from *Oryza glumaepatula* Revealed Pi68(t) as Putative Candidate Gene for Rice Blast Resistance. *Rice (New York, N.Y.)*, 13(1), 17.

Rurek M, et al. (2018) Cold and Heat Stress Diversely Alter Both Cauliflower Respiration and Distinct Mitochondrial Proteins Including OXPHOS Components and Matrix Enzymes. *International journal of molecular sciences*, 19(3).

Velez G, et al. (2016) Evidence supporting a critical contribution of intrinsically disordered regions to the biochemical behavior of full-length human HP1?. *Journal of molecular modeling*, 22(1), 12.

Ariani P, et al. (2016) Genome-wide characterisation and expression profile of the grapevine ATL ubiquitin ligase family reveal biotic and abiotic stress-responsive and development-related members. *Scientific reports*, 6, 38260.

Kurotani A, et al. (2015) In Silico Analysis of Correlations between Protein Disorder and Post-Translational Modifications in Algae. *International journal of molecular sciences*, 16(8), 19812.

Dong X, et al. (2015) Suppression of ASK? (AtSK32), a Clade III Arabidopsis GSK3, Leads to the Pollen Defect during Late Pollen Development. *Molecules and cells*, 38(6), 506.

Fan X, et al. (2015) Dynamic Alterations to α -Actinin Accompanying Sarcomere Disassembly and Reassembly during Cardiomyocyte Mitosis. PloS one, 10(6), e0129176.