

Resource Summary Report

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SIGnAL Salk Institute Genomic Analysis Laboratory

RRID:SCR_010258

Type: Tool

Proper Citation

SIGnAL Salk Institute Genomic Analysis Laboratory (RRID:SCR_010258)

Resource Information

URL: <http://signal.salk.edu/>

Proper Citation: SIGnAL Salk Institute Genomic Analysis Laboratory (RRID:SCR_010258)

Description: A biology and bioinformatics laboratory at the Salk containing the following databases: SIGnAL T-DNA Express Arabidopsis Tiling Array Transcriptome Salk Insertion Sequence Database Arabidopsis Gene ORFeome Collection Salk Homozygote T-DNA Collection High Resolution Arabidopsis Methylome Perlegen Arabidopsis Resequencing Arabidopsis GMUCT Uncapped & Cleaved Transcripts Single Feature Polymorphism Database High Resolution Arabidopsis Exosome Arabidopsis Interactome Single-base Resolution Epigenome Maps Transgenerational Inheritance of Methylation Variants Arabidopsis Cyclome Rice Functional Genomics Database Salk Arabidopsis 1,001 Genomes Arabidopsis Population Epigenomic Diversity Arabidopsis Biotic Stress Epigenome EIN3 -Ethylene Chip-seq/RNA-seq browser Soybean Epigenome Browser Human Human DNA Methylomes Human Pluripotent Cell Methylomes Human/Mouse Brain Methylomes Mouse Circadian Epigenome

Resource Type: data or information resource, database

Resource Name: SIGnAL Salk Institute Genomic Analysis Laboratory

Resource ID: SCR_010258

Alternate IDs: nlx_156910

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260804T043433+0000

Ratings and Alerts

No rating or validation information has been found for SIGnAL Salk Institute Genomic Analysis Laboratory.

No alerts have been found for SIGnAL Salk Institute Genomic Analysis Laboratory.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 271 mentions in open access literature.

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

Persello A, et al. (2025) A Mg-Chelatase Subunit I Missense Mutant in Barley Exhibits a Cold-Sensitive Phenotype Under Field Conditions. *Physiologia plantarum*, 177(4), e70434.

Kuhnert F, et al. (2025) RETICULATA1 is a plastid-localized basic amino acid transporter. *Nature plants*, 11(9), 1890.

Martínez Rivas FJ, et al. (2025) Parallel evolution of salinity tolerance in *Arabidopsis thaliana* accessions from Cape Verde Islands. *Science advances*, 11(28), eadq8210.

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.

Yang Y, et al. (2024) Ectopic enhancer-enhancer interactions as causal forces driving RNA-directed DNA methylation in gene regulatory regions. *Plant biotechnology journal*, 22(11), 3121.

Blomberg J, et al. (2024) *Pseudomonas syringae* infectivity correlates to altered transcript and metabolite levels of *Arabidopsis* mediator mutants. *Scientific reports*, 14(1), 6771.

Delplace F, et al. (2024) The receptor MIK2 interacts with the kinase RKS1 to control quantitative disease resistance to *Xanthomonas campestris*. *Plant physiology*, 197(1).

Safaeizadeh M, et al. (2024) Comparative RNA-seq analysis of *Arabidopsis thaliana* response to AtPep1 and flg22, reveals the identification of PP2-B13 and ACLP1 as new members in pattern-triggered immunity. *PLoS one*, 19(6), e0297124.

Zheng L, et al. (2024) A root cap-localized NAC transcription factor controls root halotropic response to salt stress in *Arabidopsis*. *Nature communications*, 15(1), 2061.

Ying S, et al. (2023) A stress-inducible protein regulates drought tolerance and flowering time in *Brachypodium* and *Arabidopsis*. *Plant physiology*, 191(1), 643.

Yang M, et al. (2023) Chloroplastic Sec14-like proteins modulate growth and phosphate deficiency responses in *Arabidopsis* and rice. *Plant physiology*, 192(4), 3030.

Hoernstein SNW, et al. (2023) A deeply conserved protease, acylamino acid-releasing enzyme (AARE), acts in ageing in *Physcomitrella* and *Arabidopsis*. *Communications biology*, 6(1), 61.

Lemke MD, et al. (2023) A genetic screen for dominant chloroplast reactive oxygen species signaling mutants reveals life stage-specific singlet oxygen signaling networks. *Frontiers in plant science*, 14, 1331346.

Chaomurilge , et al. (2023) Metabolic changes associated with dark-induced leaf senescence in *Arabidopsis nadk2* mutants. *Plant signaling & behavior*, 18(1), 2215618.

Zhang YF, et al. (2022) Mutation of glucose-methanol-choline oxidoreductase leads to thermosensitive genic male sterility in rice and *Arabidopsis*. *Plant biotechnology journal*, 20(10), 2023.

Ying S, et al. (2022) A phosphorus-limitation induced, functionally conserved DUF506 protein is a repressor of root hair elongation in plants. *The New phytologist*, 233(3), 1153.

Dhar S, et al. (2022) SHORT-ROOT Controls Cell Elongation in the Etiolated *Arabidopsis* Hypocotyl. *Molecules and cells*, 45(4), 243.

Ying S, et al. (2022) A novel calmodulin-interacting Domain of Unknown Function 506 protein represses root hair elongation in *Arabidopsis*. *Plant, cell & environment*, 45(6), 1796.

Blayney J, et al. (2022) Impact on *Arabidopsis* growth and stress resistance of depleting the Maf1 repressor of RNA polymerase III. *Gene*, 815, 146130.

Zhang J, et al. (2021) An Adenylate Kinase OsAK3 Involves Brassinosteroid Signaling and Grain Length in Rice (*Oryza sativa* L.). *Rice (New York, N.Y.)*, 14(1), 105.