

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: 20260829T183021+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 284 mentions in open access literature.

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

Li F, et al. (2026) Identification of QTLs and genes regulating panicle number through genome-wide association studies in *Oryza sativa* L. *Frontiers in plant science*, 17, 1806063.

Tian Y, et al. (2026) Stratification overcomes ABA-mediated seed dormancy by uncoupling RGL2/ABI5 inhibition from α -amylase expression. *Stress biology*, 6(1).

Seo JS, et al. (2026) ELF18-INDUCED LONG NONCODING RNA 19 attenuates PAMP-induced callose deposition by modulating UDP-glycosyltransferase 71B6-associated ABA levels. *Plant cell reports*, 45(2), 35.

Watanabe S, et al. (2026) The Arabidopsis NPF7.2 mediates coumarin uptake for root iron acquisition. *The New phytologist*, 250(3), 1619.

Kenny HA, et al. (2025) Navitoclax, a Bcl-2/xL Inhibitor, and YM155, a Survivin Inhibitor, in Combination with Carboplatin, Effectively Inhibit Ovarian Cancer Tumor Growth. *Molecular cancer therapeutics*, 24(8), 1252.

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.

Vinciarelli F, et al. (2025) Identification of a Specific Role of Dihydrozeatin in the Regulation of the Cell Differentiation Activity in Arabidopsis Roots. *Plants (Basel, Switzerland)*, 14(10).

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

Song X, et al. (2025) Cloning and Functional Analysis of Glyoxalase I Gene BrGLYI 13 in *Brassica rapa* L. *International journal of molecular sciences*, 26(6).

Cheng G, et al. (2025) Fatty Acid ABCG Transporter GhSTR1 Mediates Resistance to *Verticillium dahliae* and *Fusarium oxysporum* in Cotton. *Plants (Basel, Switzerland)*, 14(3).

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

Li M, et al. (2025) Dimerization-activated PP2C-D2 and D5 phosphatases negatively regulate brassinosteroid signaling by antagonizing BRI1. *Proceedings of the National Academy of Sciences of the United States of America*, 122(52), e2526122122.

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.

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

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.

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.

Yi F, et al. (2024) Positive roles of the Ca²⁺ sensors GbCML45 and GbCML50 in improving cotton *Verticillium* wilt resistance. *Molecular plant pathology*, 25(6), e13483.

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.