

Resource Summary Report

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SGN

RRID:SCR_004933

Type: Tool

Proper Citation

SGN (RRID:SCR_004933)

Resource Information

URL: <http://solgenomics.net/>

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Description: A clade oriented, community curated database containing genomic, genetic, phenotypic and taxonomic information for plant genomes. Genomic information is presented in a comparative format and tied to important plant model species such as Arabidopsis. SGN provides tools such as: BLAST searches, the SolCyc biochemical pathways database, a CAPS experiment designer, an intron detection tool, an advanced Alignment Analyzer, and a browser for phylogenetic trees. The SGN code and database are developed as an open source project, and is based on database schemas developed by the GMOD project and SGN-specific extensions.

Abbreviations: SGN, SGN ref

Synonyms: SGN ref, Sol Genomics Network

Resource Type: data or information resource, database

Defining Citation: [PMID:20935049](#), [PMID:16010005](#)

Keywords: database, clade, genomic, sequence, phenotype, pathway, genetic, taxonomy, annotation, blast, plant genome, bio.tools, FASEB list

Funding: USDA ;
ATC Inc. Advanced Technologies Cambridge ;
NSF 0116076;
NSF 9872617;
NSF 975866;
NSF 0421634

Availability: Public, The community can contribute to this resource

Resource Name: SGN

Resource ID: SCR_004933

Alternate IDs: r3d100012078, nlx_89764, biotools:sol_genomics_network

Alternate URLs: https://bio.tools/sol_genomics_network, <https://doi.org/10.17616/R3FS95>

Old URLs: <http://www.sgn.cornell.edu/>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260806T054408+0000

Ratings and Alerts

No rating or validation information has been found for SGN.

No alerts have been found for SGN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 993 mentions in open access literature.

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

Wang L, et al. (2025) A receptor antagonist counterbalances multiple systemin phytocytokines in tomato. *Cell*.

Yang Y, et al. (2025) Mitochondrial ROS trigger interorganellar signaling and prime ER processes to establish enhanced plant immunity. *Science advances*, 11(40), eady9234.

Hashmi SS, et al. (2025) Exploring the role of ATP-binding cassette transporters in tomato (*Solanum lycopersicum*) under cadmium stress through genome-wide and transcriptomic analysis. *Frontiers in plant science*, 16, 1536178.

Zhong K, et al. (2025) NbPIRIN promotes the protease activity of papain-like cysteine protease NbRD21 to inhibit Chinese wheat mosaic virus infection. *PLoS pathogens*, 21(4), e1013037.

Cao P, et al. (2025) A SIMYB78-regulated bifunctional gene cluster for phenolamide and salicylic acid biosynthesis during tomato domestication, reducing disease resistance. *Journal of integrative plant biology*, 67(7), 1947.

Koyama R, et al. (2025) Lipid transfer protein VAS inhibits the hypersensitive response via reactive oxygen species signaling in *Nicotiana benthamiana*. *Journal of experimental botany*, 76(4), 1285.

Zhao D, et al. (2025) GATA8-Mediated Antiviral Defence Is Countered by Tomato Chlorosis Virus-Encoded Pathogenicity Protein p27. *Molecular plant pathology*, 26(7), e70115.

Jo L, et al. (2025) Transcription factors SIMYB41, SIMYB92, and SIWRKY71 regulate gene expression in the tomato exodermis. *Journal of experimental botany*, 76(21), 6472.

Li L, et al. (2025) Effect of Low Red-to-Far-Red Light on Stem Elongation and Pith Cell Development in Dicots. *Plant direct*, 9(4), e70072.

Almeida J, et al. (2025) The FIBRILLIN multigene family in tomato, their roles in plastoglobuli structure and metabolism. *The Plant journal : for cell and molecular biology*, 123(5), e70447.

Paudel DB, et al. (2025) Transcriptomic changes associated with infection of *Nicotiana benthamiana* plants with tomato ringspot virus (genus *Nepovirus*) during the acute symptomatic stage and after symptom recovery. *PloS one*, 20(9), e0328517.

Razifard H, et al. (2025) The Evolutionary Dynamics of Genetic Mutational Load Throughout Tomato Domestication History. *Molecular ecology*, 34(24), e70024.

Yan D, et al. (2025) A Phase-Separated SR Protein Reprograms Host Pre-mRNA Splicing to Enhance Disease Susceptibility. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(27), e2500072.

Liu S, et al. (2025) Late blight pathogen targets host Rab-G3 GTPases with an atypical GTPase-activating protein. *Journal of integrative plant biology*, 67(8), 2135.

Zhang J, et al. (2025) Genome- and Transcriptome-Wide Characterization and Expression Analyses of bHLH Transcription Factor Family Reveal Their Relevance to Salt Stress Response in Tomato. *Plants (Basel, Switzerland)*, 14(2).

Brumm S, et al. (2025) Functional divergence of plant SCAR/WAVE proteins is determined by intrinsically disordered regions. *Science advances*, 11(21), eadt6107.

Pascual LS, et al. (2025) Multi-omics-based insights into tomato adaptation to multifactorial stress combination. *Plant physiology*, 199(3).

Yan XC, et al. (2025) Single-cell transcriptomic profiling of maize cell heterogeneity and systemic immune responses against *Puccinia polysora* Underw. *Plant biotechnology journal*, 23(2), 549.

Matuszkiewicz M, et al. (2025) Identification of genes involved in the tomato root response to *Globodera rostochiensis* parasitism under varied light conditions. *Journal of applied genetics*, 66(1), 47.

Lin W, et al. (2025) The transcriptional analysis of pepper shed light on a proviral role of light-harvesting chlorophyll a/b binding protein 13 during infection of pepper mild mottle virus. *Frontiers in plant science*, 16, 1533151.