

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: 20260821T193740+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 1261 mentions in open access literature.

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

Hamel LP, et al. (2026) Expression of a constitutively active nitrate reductase increases SARS-CoV-2 Spike protein production in *Nicotiana benthamiana* leaves that otherwise show traits of senescence. *Plant biotechnology journal*, 24(1), 204.

Van Vu T, et al. (2026) Development of an ultra-efficient prime editing system in tomato. *Nature communications*, 17(1), 95.

Kajiura H, et al. (2026) Protein-Derived Signal Peptides Induced by *Agrobacterium* Infection Promote the Secretion of Recombinant Proteins in *Nicotiana benthamiana*. *Plant biotechnology journal*, 24(1), 187.

Hajnal ??B, et al. (2026) The non-catalytic binding of auxin, cytokinin and salicylic acid by tomato Phi class glutathione transferases: insights from computational modelling. *Plant molecular biology*, 116(2), 17.

Gao H, et al. (2026) OsRNS4-mediated cross-kingdom RNA interference is inhibited by *Ustilagoidea virens* effector SCRE2 to promote infection in rice. *Science advances*, 12(6), eadx7385.

Dos Reis GL, et al. (2026) The Interplay of Light Signaling and SIAN1 Expression in Regulating Anthocyanin Accumulation in Fruit Tissues of Purple Tomatoes. *Physiologia*

plantarum, 178(1), e70740.

Wang Z, et al. (2026) Methionine Synthase Positively Regulates Plant Defence to Both RNA and DNA Viruses and Is Useful for Developing Broad-Spectrum Antiviral Resistance in Crops. *Plant biotechnology journal*, 24(6), 3821.

Ding Y, et al. (2026) A Truncated WRKY Protein Enhances Drought Resistance in Wild Tomatoes Through the SIWRKY16-CIP2b-SISYP121 Module. *Plant biotechnology journal*, 24(6), 3840.

Chaudhary R, et al. (2026) Cross-Species Reprogramming of Developmental Plasticity and Metabolic Rewiring via Banana-Derived WUS2 Developmental Regulator. *Plant biotechnology journal*, 24(6), 4174.

Pan J, et al. (2026) Genome-Wide Characterization of the Expansin Gene Family in Eggplant (*Solanum melongena* L.) Reveals Its Roles in Fruit Development and Heat Stress Response. *Plants (Basel, Switzerland)*, 15(7).

Hou H, et al. (2026) Genome-wide characterization of cytochrome P450 genes in *Solanum tuberosum* and StCYP481 role in salt tolerance. *BMC plant biology*, 26(1).

Yang Z, et al. (2026) Identification and Expression Analysis of the Goji Haploid-Inducible Gene DMP. *International journal of molecular sciences*, 27(6).

Jia L, et al. (2026) Characterization and expression analysis of UBC gene family provide insights into the potential roles in pigment biosynthesis in pepper fruit. *BMC genomics*, 27(1).

van Rengs WMJ, et al. (2026) Wild tomato genome assemblies reveal structural variants and repeat content act as recombination barriers. *Nature communications*, 17(1).

Wang L, et al. (2026) A Noncanonical Auxin-Sensing Mechanism Uncovered by Screening the Auxin Response Factor 3 Interacting Proteins in Tomato. *International journal of molecular sciences*, 27(3).

Zhang D, et al. (2026) Genome-Wide Identification of the CCCH Gene Family and Functional Exploration of MdC3H49 Under Drought Stress Response in Apple (*Malus domestica*). *Plants (Basel, Switzerland)*, 15(8).

Zhang W, et al. (2026) Epitranscriptomic profiling of cytosine N4 acetylation (ac4C) in *Solanum lycopersicum* and dynamic changes under heat stress condition. *Molecular horticulture*, 6(1).

Wang X, et al. (2026) Drought-induced SICL10 coordinates ethylene biosynthesis and root hair development to enhance osmotic stress tolerance in tomato. *Plant communications*, 7(6), 101733.

Peng D, et al. (2026) Potyviruses recruit host eIF4A3 to block m6A-mediated RNA decay by steric hindrance of viral RNA methylation in plants. *Nucleic acids research*, 54(1).

Wang Z, et al. (2026) Genome-Wide Identification and Expression Analysis of Pathogenesis-Related Protein 1 in Sweet Potato and Its Two Relatives. *Food science & nutrition*, 14(3), e71622.