About the Sol Genomics Network

The Sol Genomics Network (SGN) is a clade-oriented database dedicated to the biology of the Solanaceae family which includes a large number of closely related and many agronomically important species such as tomato, potato, tobacco, eggplant, pepper, and the ornamental *Petunia hybrida*.

SGN is part of the International Solanaceae Initiative (SOL), which has the long-term goal of creating a network of resources and information to address key questions in plant adaptation and diversification.

A key problem of the post-genomic era is the linking of the phenome to the genome, and SGN allows to track and help discover new such linkages.

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| **Data** |   |

**Solanaceae and other Genomes**

SGN is a home for Solanaceae and closely related genomes, such as selected Rubiaceae genomes (e.g., *Coffea*). The [tomato](https://solgenomics.net/organism/Solanum_lycopersicum/genome), [potato](https://solgenomics.net/organism/Solanum_tuberosum/genome), [pepper](https://solgenomics.net/organism/Capsicum_annuum/genome), and [eggplant](https://solgenomics.net/organism/Solanum_melongena) genome are examples of genomes that are currently available. If you would like to include a Solanaceae genome that you sequenced in SGN, please [contact us](https://solgenomics.net/contact/form).

**ESTs**

SGN houses EST collections for tomato, potato, pepper, eggplant and petunia and corresponding unigene builds. EST sequence data and cDNA clone resources greatly facilitate cloning strategies based on sequence similarity, the study of syntenic relationships between species in comparative mapping projects, and are essential for microarray technology.

**Unigenes**

SGN assembles and publishes unigene builds from these EST sequences. For more information, see [Unigene Methods](https://solgenomics.net/methods/unigene/index.pl).

**Maps and Markers**

SGN has genetic maps and a searchable catalog of markers for tomato, potato, pepper, and eggplant.

**Tools**

SGN makes available a wide range of web-based bioinformatics tools for use by anyone, listed [here](https://solgenomics.net/tools/). Some of our most popular tools include [BLAST](https://solgenomics.net/tools/blast/) searches, the [SolCyc biochemical pathways database](https://solgenomics.net/tools/solcyc/), a [CAPS experiment designer](https://solgenomics.net/tools/caps_designer/caps_input.pl), an [Alignment Analyzer](https://solgenomics.net/tools/align_viewer/) and [browser for phylogenetic trees](https://solgenomics.net/tools/tree_browser/). The [VIGS tool](http://vigs.solgenomics.net/) can help predict the properties of VIGS (Viral Induced Gene Silencing) constructs.

The data in SGN have been submitted by many different research groups around the world which are acknowledged on the corresponding pages on SGN. If you have data you would like to submit for display on SGN, please use the [contact us](https://solgenomics.net/contact/form) web form.

For more information about SGN datasets, see the [SGN Data Overview](https://solgenomics.net/content/sgn_data.pl). Entire datasets can also be downloaded from our FTP site.

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| **SGN community-driven gene and phenotype database** |   |

* We have developed simple web interfaces for the SGN user-community to submit, annotate, and curate the Solanaceae locus and phenotype databases. Our goal is to share biological information, and have the experts in their field review existing data and submit information about their favorite genes and phenotypes.
* Please read more about the [phenome database](https://solgenomics.net/phenome/index.pl) and how to submit information to SGN.