Resource Summary Report

Generated by dkNET on Sep 9, 2026

GeneFarm

RRID:SCR_007674
Type: Tool

Proper Citation

GeneFarm (RRID:SCR_007674)

Resource Information

URL: http://urgi.versailles.inra.fr/Genefarm/

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Description: GeneFarm is a database of structural and functional annotation of plant gene and protein families. The goal of the GeneFarm project is to obtain homogeneous, reliable, documented and traceable annotations for plant nuclear genes and gene products and to enter them into added-value database. The improved annotation will allow better data mining of the plant genomes (mainly Arabidopsis thaliana), and more secure planning and design of experiments. It is also a necessary step for building knowledge management tools for integrating plant genomic data, either for plant breeding or to get a broader interactive view of plant biological processes, like gene interaction networks. This re-annotation project, launched is mainly focused on gene families. A complete annotation pipeline using the most efficient prediction tools has been defined. The involved partners, each contributing with genes from his/her field of expertise, have exhaustively annotated families of homologous genes. A database named GeneFarm (Gene Families for Arabidopsis Management) gathers all these expert-curated annotations of plant gene families. Furthermore, collaboration with the Swiss Institute of Bioinformatics is underway to integrate the GeneFarm data into the protein knowledgebase Swiss-Prot.

Synonyms: GeneFarm

Resource Type: data or information resource, database

Keywords: plant gene, plant nuclear gene, plant protein

Resource Name: GeneFarm

Resource ID: SCR_007674

Alternate IDs: nif-0000-02881

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260905T133142+0000

Ratings and Alerts

No rating or validation information has been found for GeneFarm.

No alerts have been found for GeneFarm.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Liu L, et al. (2026) Ginsenoside compound K up-regulates ??-subunits of long-chain L-3-hydroxyacyl-CoA (HADHB) to promote fatty acid oxidation recovery and improve the balance of macrophage polarization in mice with ulcerative colitis. British journal of pharmacology, 183(13), 3633.

Coulibaly I, et al. (2008) Bioinformatic tools for inferring functional information from plant microarray data II: Analysis beyond single gene. International journal of plant genomics, 2008, 893941.