

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

FLAGdb++

RRID:SCR_007659

Type: Tool

Proper Citation

FLAGdb++ (RRID:SCR_007659)

Resource Information

URL: <http://urgv.evry.inra.fr/projects/FLAGdb++/HTML/index.shtml>

Proper Citation: FLAGdb++ (RRID:SCR_007659)

Description: A database for the functional analysis of the Arabidopsis genome. The ultimate objective of this project is to develop a database and associated bioinformatics tools based on the integration of genomic data around a selection of plant complete genomes. This tool will help users to understand the biological role of plant genes by considering them in a wide context: a multigene family, a topological environment, and/or a functional network. The database and the associated user-friendly interface is developed with a conceptual effort for the graphical display and the hierarchical organization of the data. The running integration involves the structural and functional international annotations, EST from different plant species, novel gene predictions, mutant tags, gene families, protein motifs, transcriptome data, repeat sequences, primers and tags for genomic approaches (DNA chips, synteny studies, BAC library screening, RT-PCR, SNP discovery, ...), subcellular targeting, secondary structures, 3D models, MPSS tags, curated annotations and mutant phenotypes.

Synonyms: FLAGdb++

Resource Type: data or information resource, database

Keywords: arabidopsis, arabidopsis genome, plant genome

Resource Name: FLAGdb++

Resource ID: SCR_007659

Alternate IDs: nif-0000-02840

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260821T193822+0000

Ratings and Alerts

No rating or validation information has been found for FLAGdb++.

No alerts have been found for FLAGdb++.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Smit SJ, et al. (2021) Seeing the Forest through the (Phylogenetic) Trees: Functional Characterisation of Grapevine Terpene Synthase (VviTPS) Paralogues and Orthologues. *Plants* (Basel, Switzerland), 10(8).

Smit SJ, et al. (2019) Linking Terpene Synthases to Sesquiterpene Metabolism in Grapevine Flowers. *Frontiers in plant science*, 10, 177.

Creff A, et al. (2019) A stress-response-related inter-compartmental signalling pathway regulates embryonic cuticle integrity in Arabidopsis. *PLoS genetics*, 15(4), e1007847.

Farjad M, et al. (2018) Nitrogen Limitation Alters the Response of Specific Genes to Biotic Stress. *International journal of molecular sciences*, 19(11).

Chen NWG, et al. (2018) Common Bean Subtelomeres Are Hot Spots of Recombination and Favor Resistance Gene Evolution. *Frontiers in plant science*, 9, 1185.

Chen X, et al. (2017) Dek35 Encodes a PPR Protein that Affects cis-Splicing of Mitochondrial nad4 Intron 1 and??Seed Development in Maize. *Molecular plant*, 10(3), 427.

Zhu BQ, et al. (2014) Identification of a plastid-localized bifunctional nerolidol/linalool synthase in relation to linalool biosynthesis in young grape berries. *International journal of molecular sciences*, 15(12), 21992.

Colcombet J, et al. (2013) Systematic study of subcellular localization of Arabidopsis PPR proteins confirms a massive targeting to organelles. *RNA biology*, 10(9), 1557.

Houel C, et al. (2010) Patterns of sequence polymorphism in the fleshless berry locus in cultivated and wild *Vitis vinifera* accessions. *BMC plant biology*, 10, 284.