

# Gene coexpression database for plants

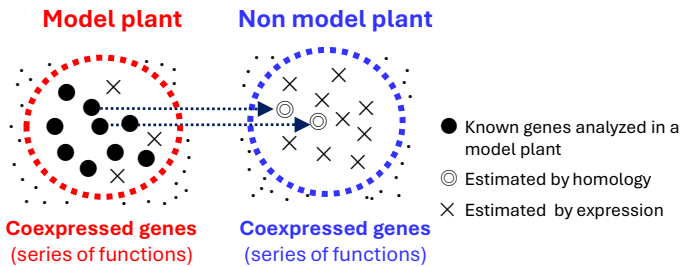


ATTEO-II

<https://atted.jp/>



ATTEO-II was launched in Nov 2004 as a database for searching for and analyzing co-expressed genes. Since groups of genes that are expressed in coordination under specific conditions often play a role in a series of physiological functions, it is thought that co-expression relationships will allow us to understand the functional groupings and complex regulatory relationships of genes.



ATTEO-II v13 contains gene co-expression information for 19 species and 20 plant strains.

It also includes tools for investigating the conditions and environmental factors that lead to the co-expression of a target gene, examining the physiological function of that gene and its regulatory relationships, and comparing and analyzing co-expressed genes across different species.

## <Dicotyledonous plants>

- *Arabidopsis thaliana* (Arabidopsis)
- *Solanum lycopersicum* (Tomato)
- *Medicago truncatula* (Medicago)
- *Glycine max* (Soybean)
- *Populus trichocarpa* (Poplar)
- *Vitis vinifera* (Grape)
- *Brassica napus* (Field mustard)
- *Gossypium hirsutum* (Upland cotton)
- *Solanum tuberosum* (Potato)
- *Nicotiana tabacum* (Tobacco)
- *Citrus sinensis* (Orange)

## <Monocot>

- *Oryza sativa subsp. japonica* (Japonica rice)
- *Oryza sativa subsp. indica* (Indica rice)
- *Zea mays* (Maize)
- *Triticum aestivum* (Wheat)
- *Hordeum vulgare* (Barley)
- *Sorghum bicolor* (Sorghum)
- *Brachypodium distachyon* (Brachypodium)

## <Green algae>

- *Chlamydomonas reinhardtii* (Chlamydomonas)

ATTEO-II ver.13.0

ATTEO-II provides co-regulated gene relationships to estimate gene functions

All words [Search]

**Search**  
• GeneTable  
• EdgeAnnotation  
• CoExSearch  
• etc.

**Draw**  
• NetworkDrawer  
• HCluster  
• CoexViewer  
• etc.

**Browse**      **Bulk download**

**Target species with page examples**

Arabidopsis [coex][map][PC View]	Field mustard [coex][map][PC View]	Soybean [coex][map][PC View]
Medicago [coex][map][PC View]	Rice [coex][map][PC View]	Poplar [coex][map][PC View]
Tomato [coex][map][PC View]	Grape [coex][map][PC View]	Maize [coex][map][PC View]
Wheat [coex][map][PC View]	Barley [coex][map][PC View]	Upland cotton [coex][map][PC View]
Rapeseed [coex][map][PC View]	Chlamydomonas [coex][map][PC View]	Sorghum [coex][map][PC View]
Potato [coex][map][PC View]	Orange [coex][map][PC View]	Stiff brome [coex][map][PC View]
Tobacco [coex][map][PC View]		

statistics

Figure 1: ATTEO-II v13 Homepage

In addition to links to search functions such as GeneTable, EdgeAnnotation, and CoExSearch (Search) and analysis functions such as NetworkDrawer, CoexMap, and Hcluster (Draw), there are also links to main sample pages for each of the 19 species and 20 strains of plants included (Target Species with page examples) and a link to the download page (Bulk download).

ATTEO-II was supported from 2022 to 2025 under the project of JST Database Integration Coordination Program (DICP) "Platform of gene network information for non-model plants (PI: Takeshi Obayashi, Professor, Tohoku University)"

# Analysis functions implemented in ATTED-II



ATED-II

<https://atted.jp/>



## Analytical Functions Implemented in ATTED-II

Based on the results of principal component analysis of co-expressed genes, you can investigate the conditions and environmental factors under which target genes are co-expressed, as well as the physiological functions they perform and their regulatory relationships. You can also perform comparative analyses of co-expressed genes across different species.

### Understanding the Overall Structure of Co-expression

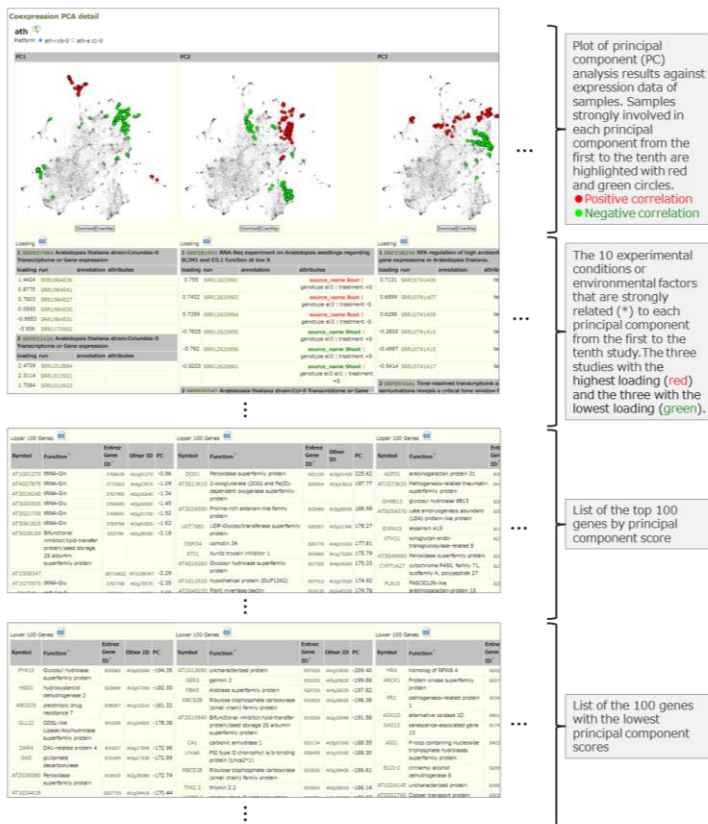
- **CoexMap:** A tool that displays any number of genes on a species-level co-expression map, allowing users to grasp the overall structure.

### Examining the Detailed Functions of Co-expressed Genes

- **CoexViewer:** A tool that examines the conditions under which any given gene pair co-expresses (or does not co-express) based on the variation patterns of principal components.
- **PC View:** A tool designed to support CoexViewer, presenting the relationship between cellular environments and gene functions as grouped by each principal component.

### Identifying Functional Differentiation

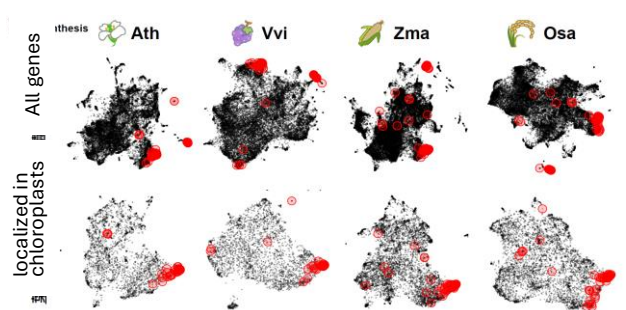
- **NetworkDrawer:** A tool that combines co-expression (expression similarity) with paralog information (sequence similarity) to present the data.



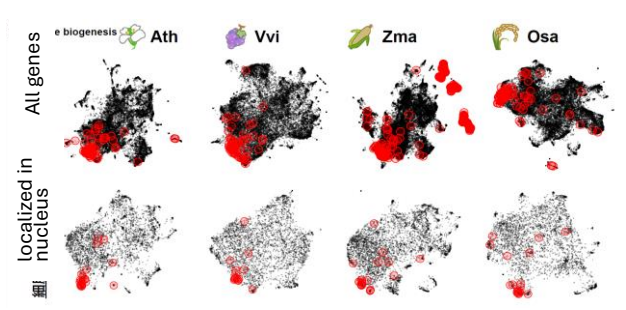
**Figure 2: Example of PC View (Arabidopsis thaliana)**

- (1) Results of principal component analysis of sample expression data.
- (2) Conditions that strongly contribute to each of the first 10 principal components.
- (3) List of the top 100 genes by principal component score.
- (4) List of the 100 genes with the lowest principal component scores.

(A) Photosynthesis-related genes localized in chloroplasts



(B) Genes involved in ribosome biosynthesis localized to the nucleus



**Figure 3: Cross-species Comparative Analysis Tool**  
(CoexMap at the organelle level)

Inter-plant comparison of genes co-expressed in chloroplasts (A) and the cell nucleus (B). From left to right: Arabidopsis thaliana (Ath), grapevine (Vvi), maize (Zma), and rice (Osa). Co-expression map of genes encoding proteins localized to all genes (top panel) and organelles (bottom panel). The red circles in (A) indicate photosynthesis-related genes (KEGG:00195). The red circles in (B) indicate ribosome biosynthesis-related genes (KEGG:03008). While no consistent localization pattern is observed for all genes, focusing on each organelle reveals a consistent distribution across species.