

# Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

## FuncExpression

RRID:SCR\_005773

Type: Tool

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### Proper Citation

FuncExpression (RRID:SCR\_005773)

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### Resource Information

**URL:** <http://www.plexdb.org/plex.php?database=Barley/funcexpression.php>

**Proper Citation:** FuncExpression (RRID:SCR\_005773)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 11, 2012. FuncExpression is a web-based resource for functional interpretation of large scale genomics data. FuncExpression can be used for the functional comparison of plant, animal, and fungal gene name lists generated from genomics and proteomics experiments. Multiple gene lists can be classified, compared and visualized. FuncExpression supports two way-integration of plant gene functional information and the gene expression data, which allows for further cross-validation with plant microarray data from related experiments at BarleyBase. Platform: Online tool

**Abbreviations:** FuncExpression

**Resource Type:** data analysis service, service resource, analysis service resource, production service resource

**Keywords:** statistical analysis, genomics, compare, function, plant, animal, fungus, gene, proteomics, gene expression, microarray

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** FuncExpression

**Resource ID:** SCR\_005773

**Alternate IDs:** nlx\_149237

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260810T040417+0000

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### Ratings and Alerts

No rating or validation information has been found for FuncExpression.

No alerts have been found for FuncExpression.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.