# Introduction to PLAZA, a resource for plant comparative genomics

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| **Objective** |  | Browse plant genomics data using the PLAZA platform and analyze a smallexperimental gene set using the Workbench |

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| **Part I** |  | Introduction PLAZA platform  |
| **Part II** |  | Working with the PLAZA website.In order to get the users to know the platform, we’ll try to start with as little ‘input data’ as possible, and rather go from page to page indicating the connectivity within the PLAZA platform.**PLAZA Website:*** http://bioinformatics.psb.ugent.be/plaza/

**INPUT 1: genes, gene families and functional annotation*** Go to gene page of Arabidopsis thaliana gene AT2G41430
* What is the function of this gene? Does the description of the gene match the associated functional annotation?
* What kinds of sequences are available for this gene?
* What is the associated gene family for the Arabidopsis thaliana gene?
* Are the Arabidopsis thaliana and lyrata genes adjacent in the phylogenetic tree associated with this gene family?
* In what sub family is the gene present? What is the function of the sub family?
* Find the orthologs of this gene in apple and maize, using the Integrative Orthology method.

**INPUT 2: Locating gene families using GO*** Search the GO term with description “response to molecule of fungal origin”
* What are the associated gene families with this GO term?
* What are the general InterPro domains associated with these gene families?

**INPUT 3: Using the PLAZA workbench*** Create workbench account.
* Use the workbench to upload a set of Arabidopsis thaliana genes (mapped from pepper sequences). Dataset name: input\_genes\_ath.txt
* Is the data-set enriched for a certain GO-term?
* Locate the orthologous genes for this data-set (using at least 3 types of evidence) in Zea mays.
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