Submitting GO and PO annotations using TOAST.

If you are a registered TAIR user, you can use the TAIR Online Annotation Submission Tool (TOAST) to make Gene Ontology and Plant Ontology annotations based on experimental data from publications. Any registered user can annotate gene function from published works, you do not need to be the author.

Community contributed annotations are displayed on TAIR detail pages and attributed to the submitter. GO/PO annotations are also included TAIR data releases and GO annotations are sent to the Gene Ontology Consortium along with TAIR curated GO annotations, where they are freely available to the public.

Some useful resources before you start

- TAIR registration help
- TOAST Tutorial (YouTube)
- Understanding GO annotations

Before entering data, ensure that there is ample time to complete and submit the form. TOAST does not save work in progress. If it is necessary to stop or close the browser, it is best to submit whatever annotations you have completed to avoid losing the data.

1. Enter your TAIR username and password. You must be registered with TAIR in order to submit data via TOAST.

2. On the resulting data entry form enter the PubMed ID or Digital Object Identifier (DOI) for the article you wish to annotate.

   TAIR only displays annotations from published works. You may submit annotations for articles that have been accepted for publication that have received a temporary DOI but TAIR does not accept annotations for unpublished work.

3. Enter the AGI locus identifier (e.g. At1g01010) of the first gene you wish to annotate. Start by typing in the name and the autocomplete function will suggest possible completions. At this point you can also enter in any symbolic name(s) to associate to the locus.

4. Enter the annotations. The form contains separate sections for each type of annotation (GO Molecular Function, GO Process, Expression). At least one annotation must be entered order to be able to submit (otherwise the Submit button remains grayed out).
   a. Enter the term in the left column. The auto-suggest function will offer a list of suggested terms. Choose one of the suggested terms, or if none is appropriate, enter a new term.

      A TAIR curator will review all the contributions and will approve the annotation, update to find the best term that matches, or determine if a new ontology term needs to be added.

   b. Enter the supporting evidence in the right column. All annotations must be backed up by evidence. Choose the evidence type from the dropdown menu that most closely fits the experimental method.

5. To add additional annotations for any category click on the small green plus sign to the right. For example to add an additional molecular function annotation click the plus sign (+) to the right of the annotation.
row and a new data entry row will appear. To delete an annotation, click on the red X to the right of the annotation row.

6. Enter comments. At the bottom of the form there is a section to enter comments that may include information that cannot be captured in a GO or PO annotation. This section is optional.

7. Submit the annotations or add another gene. Once all of the annotations for the gene entered in step 5 are done, either submit the annotations or annotate another gene described in the same paper.
   a. To add another gene, go to the top of the form and click on the plus sign (+) in the upper right corner. This will append a new gene entry form to the bottom of the page.
   b. To submit annotations, click on the Submit Annotations button on the lower left side of the page.

8. Once the data is submitted a curator will review the submission. If there are any questions, a curator will contact the submitter. It can take a week or two before the data is visible in TAIR.