

# 2023-04-27: CALL FOR PARTICIPATION - Manual Review

Thank you for your interest in participating in the manual review phase of the V12 reannotation project.

- **Task:** Review the structure (introns, exons, boundaries, sequence) of a set of genes and either validate or update the structures and sequence when needed. Depending on how many participants sign up, the total number of genes per person is estimated between 100 and 200.
- **Tool/Training:** [Apollo](#) hosted by TAIR. All participants will attend a mandatory training session and will create user accounts to track their work.
- **Assignment:** Gene sets will be assigned either on stated expertise or type of gene change (new to v12, deleted in v12, split, merged).
- **Deadline:** We need people to complete their lists within two months of the start of curation. Weekly reports will be centrally created to track progress.
- **Time Commitment:** Expect to spend 30 minutes per gene, especially in the beginning as you are getting used to the tool. That could be up to 100 hrs of work. Over two months, that's just over an hour a working day.
- **Review:** At least a subset of genes that are curated by each participant will be reviewed by a second participant.
- **Rewards:** Experience in structural annotation and co-authorship in the publication that will describe the v12 project and its results.

**We will follow up by email to schedule training.**

## **Action:**

1. Spread the word and share the call for participation with people in your lab/network.
2. If you can participate yourself, [fill out this form](#) to join the team.
3. If you cannot access the Google Form, please send an email to <curator@arabidopsis.org> with the following information:
  - Name
  - Email address
  - Institution
  - Time zone where you work (to aid setting up the training session times)
  - Area of interest for manual review (please specify area or enter 'any set of genes is fine')
  - Experience in structural annotation review (yes/no)

## **Reading materials:**

- Apollo: Democratizing genome annotation
  - <https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1006790>
- Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens (see: 'Lessons Learnt for Future Collaborative Annotation Projects' section)
  - <https://www.frontiersin.org/articles/10.3389/fmicb.2019.02477/full>