

IMG ER & MER Submission User Guide

February 2017

Log In

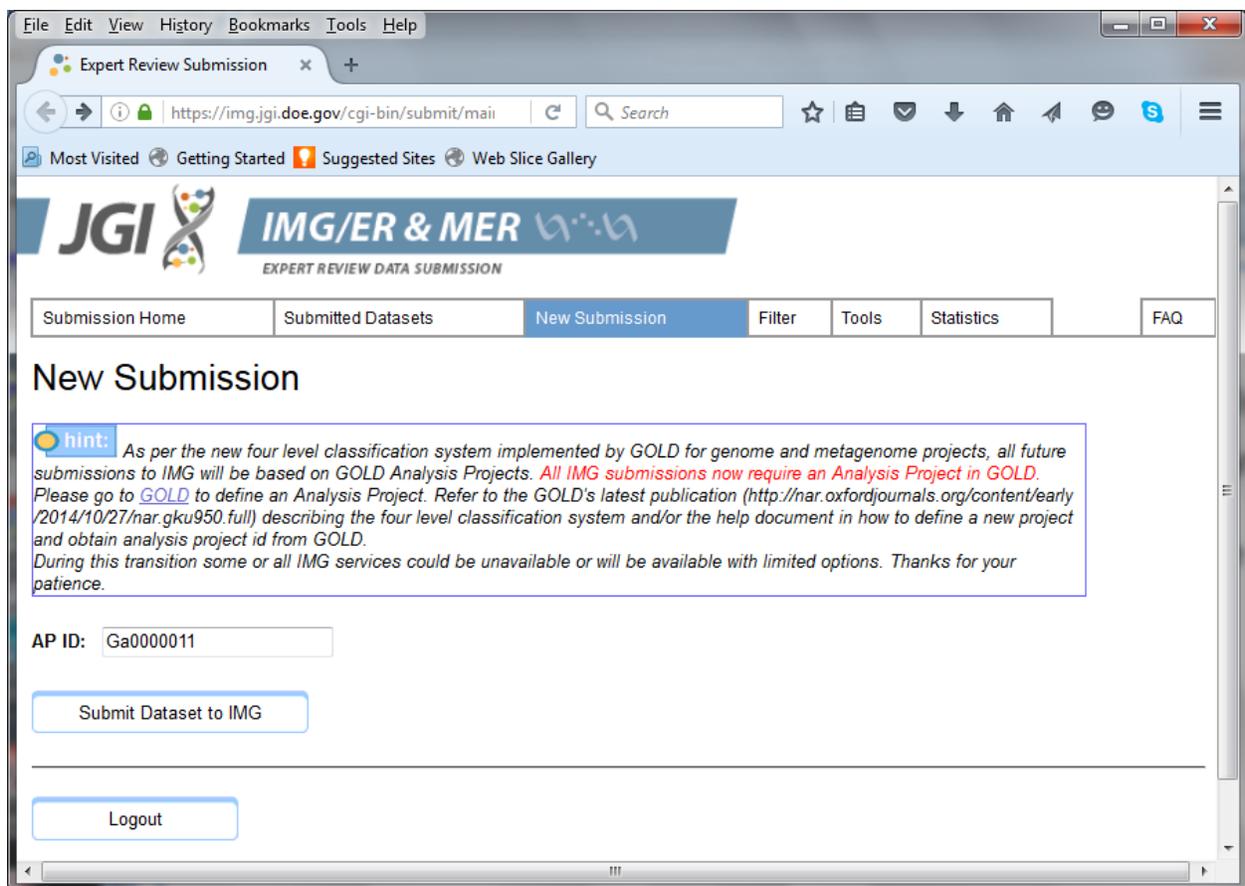
All users are required to have a JGI Single Sign On (SSO) account.

If you don't have a JGI SSO account, please go here (<http://contacts.jgi-psf.org/registration/new>) to request one. After you obtain SSO account, please use the account to log into IMG ER (<http://img.jgi.doe.gov/mer/>) to request a corresponding IMG account.

New Submission

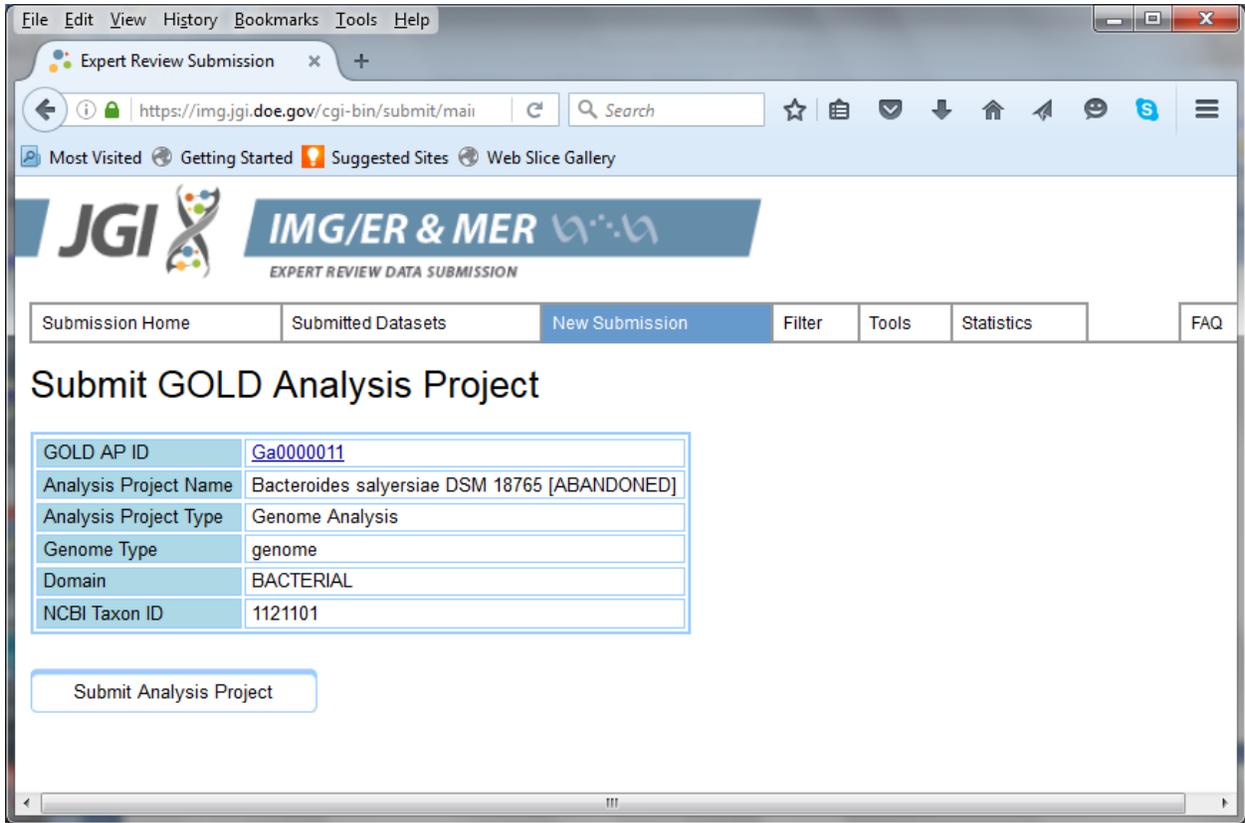
Each new submission needs to have a corresponding GOLD Analysis Project ID. Therefore, your first step is to go to GOLD (<https://gold.jgi.doe.gov/index>) to create an analysis project.

Once the GOLD analysis project is defined, you can continue the new submission by selecting "New Submission" menu from the IMG Submission UI:



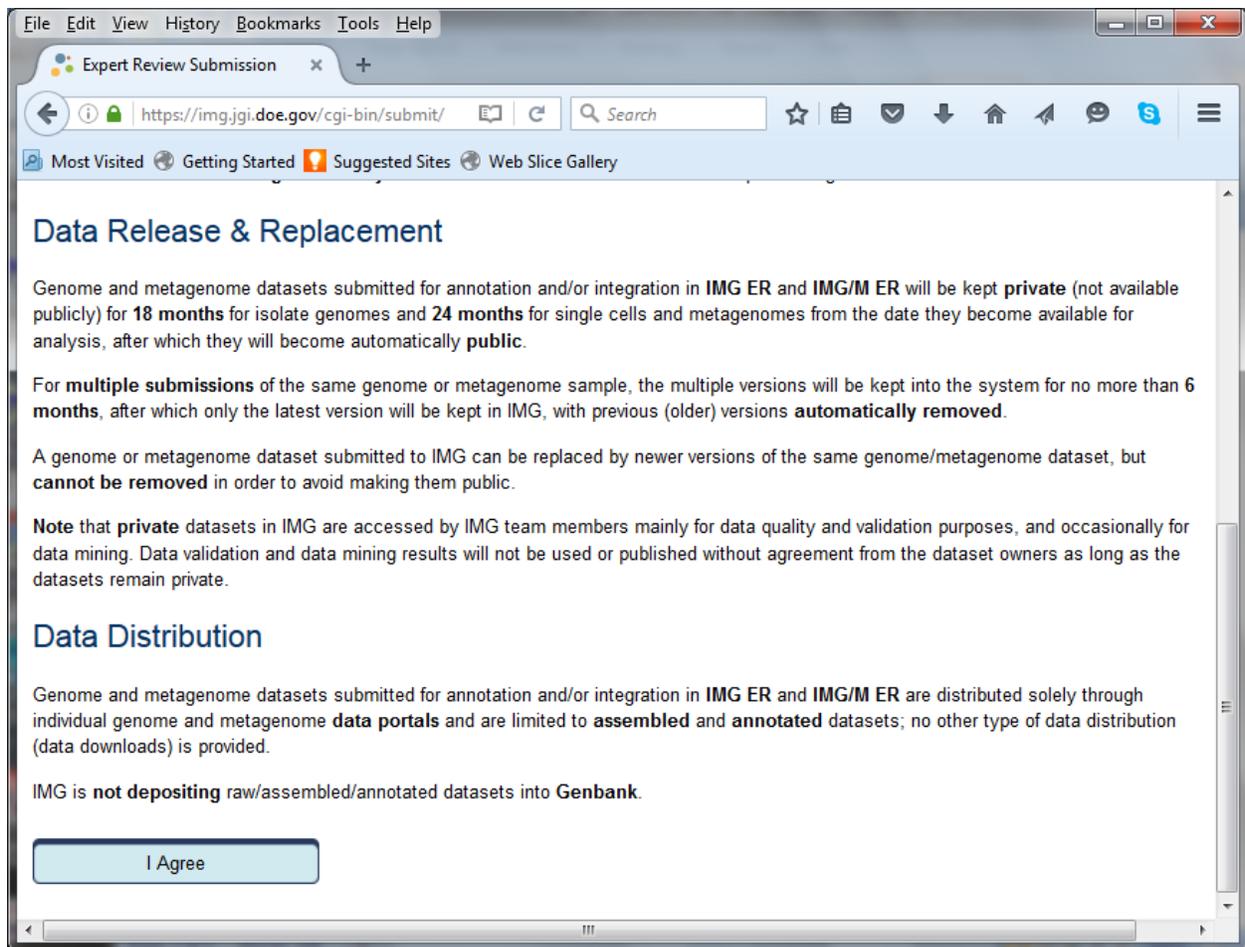
Enter the GOLD Analysis Project ID in the "AP ID" field, and click "Submit Dataset to IMG" button.

The next screen will show a short definition of this AP. If this AP is eligible for submission, there will be a "Submit Analysis Project" button shown below the project definition. If the AP has already been submitted, then there will be an error message.



Click the "Submit Analysis Project" button to continue your submission.

The next screen shows "IMG Expert Review Submission Agreement." Click "I Agree" to continue.



Depending on the GOLD AP definition, a submission can go to IMG ER (for isolate or single cell genomes) or go to IMG/M ER (for metagenomes).

Isolate or Single Cell Genome Submission

There are 4 tabs in this submission form.

Submission Information

This tab contains all basic submission information:

- Submission project: This is the analysis project name.
- GOLD ID: GOLD AP ID.
- Subtitle: An optional free text subtitle that will be appended to the project name.
- Target ER System: IMG ER.
- Is public in IMG databases? Default is "No," which means that it is a private submission available only for submitter/PI. Change the selection to "Yes" will make the submission available to all IMG users.
- Sequencing Status: Draft (this is a draft genome), Finished (this is a finished genome), Permanent Draft (this is a good draft genome; there is no plan to further complete the genome).

- Replacing Taxon OID: Enter an existing IMG Taxon OID if the new submission will replace the older genome.
- Genbank ID: Genbank accession ID (if any).

Submit annotated file

Upload a Genbank format file if you wish to submit without gene calling. Otherwise, leave this field blank, and use the "Submit sequence file" to be described immediately below.

Submit sequence file

This option allows users to upload a fasta sequence file.

- Assembled sequence: Upload fasta file here.
- Assembler used: Enter assembler information (if any).
- Sequence coverage file for assembled sequences: This option is for metagenomes only. It contains the read depth coverage file.
- Topology: linear or circular (for finished genomes)

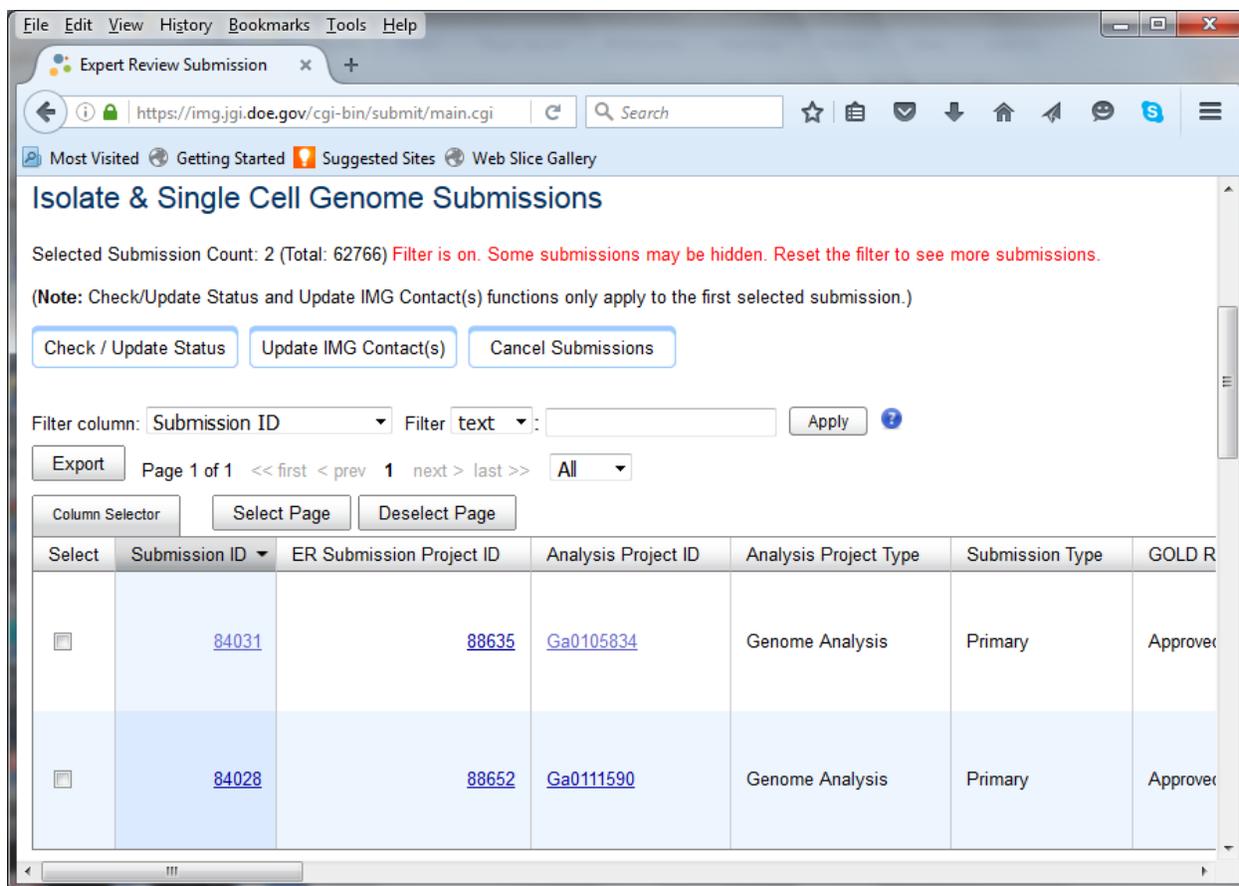
Metagenome Submission

Metagenome submission is similar to isolate genome submission except that we only support the "Submit sequence file" option for metagenomes.

Click the "Submit" button at the end of the page to finish your submission.

Check Submitted Datasets

Click on the "Submitted Datasets" menu to view your existing submissions.



You can monitor your submissions by checking the "Status" column.

If the status shows any errors, click on the submission ID to find out more details. There can be an **Error File** hyperlink for the validation log. You can resubmit your data file after you fix all the errors.

Isolate genomes are loaded into IMG about every two weeks. Metagenomes are processed constantly. JGI submissions have priority over non-JGI submissions. When there is a large batch of JGI metagenome submissions, external submissions may be delayed for a couple months.

Please note that only approved submissions will be processed. If your submission has approval status 'pending review,' please also check the GOLD Review Status of your GOLD Analysis Project. GOLD Review Status 'In Review' means that the project has not been approved by the GOLD Group. If your submission has approval status 'missing metadata,' please check **Metadata Requirements** section at the Home page. We will not answer individual email re. when a submission will be loaded.

Filtering Submissions

If you have submitted large amount of datasets into IMG, the Submitted Datasets table will be very long. You can filter out the list display by using a filter. Click on the "Filter" tab to specify your filtering condition and then click the "Apply Submission Filter" button at the end to apply the new filter.

Any Questions?

There is a "FAQ" menu item at the right upper corner of Submission UI. Please check FAQ first before sending us any emails. You can find out how to share your private genomes with colleagues, and how to release your private genomes in the FAQ.