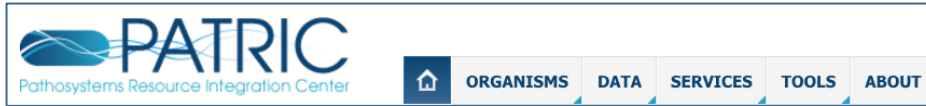
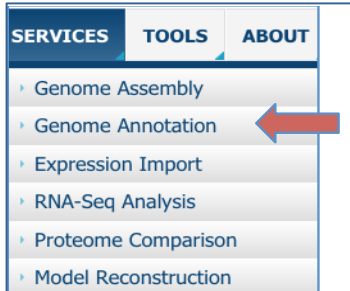


1. At the top of any PATRIC page, find the Services tab.



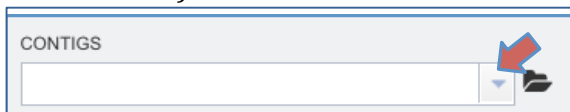
2. Click on Genome Annotation.



3. This will open up the landing page where you can annotate your genome.

The image shows the "Genome Annotation" landing page. At the top, it says "Genome Annotation" and "Annotates genomes using RASTtk." Below this is a "Parameters" section with an information icon. The parameters are: "CONTIGS" (empty text box with a dropdown arrow and folder icon), "GENOME NAME" (text box containing "My bacillus cereus"), "DOMAIN" (dropdown menu with "Bacteria" selected), "TAXONOMY RANK/NAME" (dropdown menu with "e.g. species Bacillus Cereus" selected), "TAXONOMY ID" (empty text box with a dropdown arrow), "GENETIC CODE" (dropdown menu with "11 (Archaea & most Bacteria)" selected), and "OUTPUT FOLDER" (empty text box with a dropdown arrow and folder icon). At the bottom of the form are "Reset" and "Annotate" buttons.

4. First, you have to upload contigs, either from an assembly job that you did in PATRIC, or somewhere else. In this example we are uploading a job that we submitted to the PATRIC assembly service. To submit it for annotation, click on the down arrow that follows the text box underneath Contigs (indicated by the red arrow below).



5. This will open up a drop-down box that will show you all the assemblies that you currently have in PATRIC. Click on the one that you are interested in annotating.

Parameters ⓘ

CONTIGS

contigs.fa

/home/.../Brucella suis bv 2 Hungary/
12_2.idba_contigs.fa

/home/.../Brucella suis bv 2 Hungary/
12_3.velvet_contigs.fa

/home/.../Brucella suis bv 2 Hungary/
12_1.spades_contigs.fasta

/home/.../Brucella melitensis F3_99_548_spades/
Brucella melitensis F3_99_548_spades.contigs.fasta

/home/.../Brucella melitensis_F3_99_548_velvet/
Brucella melitensis_F3_99_548_velvet.contigs.fasta

/home/.../Brucella melitensis_F3_99_548_contigs/
Brucella melitensis_F3_99_548_contigs.contigs.fasta

6. Now you will need to write in the name of your genome. The name should be something specific

Parameters ⓘ

CONTIGS

GENOME NAME
My bacillus cereus

DOMAIN
Bacteria

TAXONOMY RANK/NAME
e.g. species Bacillus Cereus

TAXONOMY ID

GENETIC CODE
11 (Archaea & most Bacteria)

OUTPUT FOLDER

GENOME NAME
Brucella melitensis_F3_99_548

7. I find it easiest to fill in the Taxonomy ID before filling in the field for Taxonomy Rank/Name. The taxonomy ID for Brucella melitensis is 29459. When you type that in, you'll notice that a line appears below with the ID and species name. Click on that line.

Parameters ⓘ

CONTIGS

GENOME NAME
My bacillus cereus

DOMAIN
Bacteria

TAXONOMY RANK/NAME
e.g. species Bacillus Cereus

TAXONOMY ID

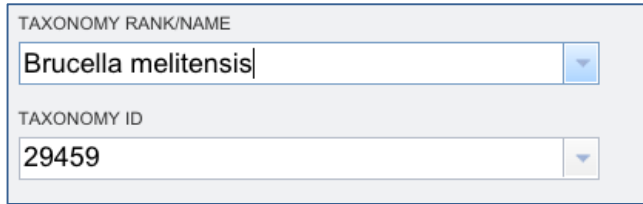
GENETIC CODE
11 (Archaea & most Bacteria)

OUTPUT FOLDER

TAXONOMY ID
29459

29459 [Brucella melitensis]

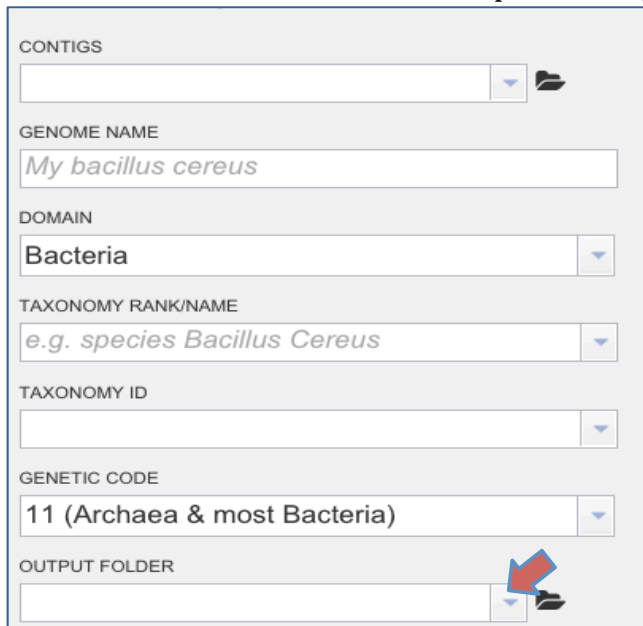
8. That will autofill the Taxonomy Rank/Name.



TAXONOMY RANK/NAME
Brucella melitensis

TAXONOMY ID
29459

9. Next you will need to assign an Output Folder. Click on the down arrow that follows the text box underneath Output folder (indicated by the red arrow below).



CONTIGS

GENOME NAME
My bacillus cereus

DOMAIN
Bacteria

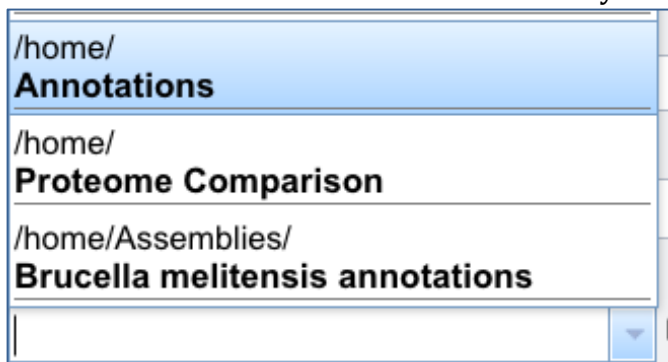
TAXONOMY RANK/NAME
e.g. species Bacillus Cereus

TAXONOMY ID

GENETIC CODE
11 (Archaea & most Bacteria)

OUTPUT FOLDER

10. This will open up a drop down box that shows your folder. You can put it wherever you like, but in this example we will store this annotation in the Annotations folder. You choose the folder by clicking on it.



/home/
Annotations

/home/
Proteome Comparison

/home/Assemblies/
Brucella melitensis annotations

11. Whatever you clicked on will show up in the text box.

OUTPUT FOLDER

Annotations

12. Once you've filled everything in, you're ready to start the annotation job. You can do this by clicking on the Annotate button (indicated by the red arrow below).

Parameters ⓘ

CONTIGS
Brucella melitensis_F3_99_548_cont

GENOME NAME
Brucella melitensis_F3_99_548

DOMAIN
Bacteria

TAXONOMY RANK/NAME
Brucella melitensis

TAXONOMY ID
29459

GENETIC CODE
11 (Archaea & most Bacteria)

OUTPUT FOLDER
Annotations

Reset Annotate

13. A message will appear below the box that indicated that your job is now in the queue.

Annotation Job has been queued.

14. You can check the status of your annotation job by clicking on the Jobs indicator at the bottom of the PATRIC page.

Uploads 0·0 Jobs 43·1·0·7

15. Clicking on Jobs will take you to the Jobs Status page, where you can see how your assembly job is progressing. You can also see the status of all the previous service jobs that you have submitted to PATRIC.

● in-progress	11/20/15, 10:47 AM	GenomeAnnotation	Brucella melitensis_F3_99_548	11/20/15, 10:47 AM	
● completed	11/18/15, 1:27 PM	GenomeAnnotation	Brucella melitensis_F3_99_548_velvet	11/18/15, 1:27 PM	11/18/15, 1:38 PM