

# Running "16sblaster" at iPlant

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## Abstract

See upcoming paper by Watts, Hurwitz, Youens-Clark.

Code is freely available at [Github](#).

**Citation:** Ken Youens-Clark Running "16sblaster" at iPlant. **protocols.io**

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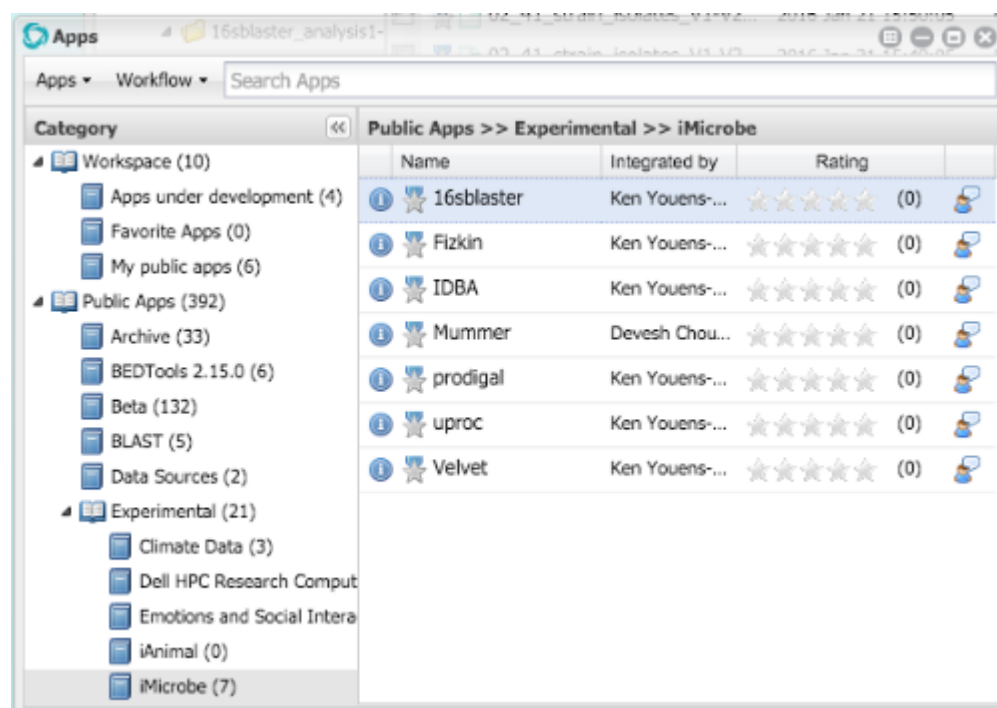
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## Protocol

### Step 1.

Go to [the 16sblaster app](#).

Alternately, login to the iPlant/CyVerse Discovery Environment. Choose the "Apps" button on the left, then navigate to "Public Apps -> Experimental -> iMicrobe." Click on the "16sblaster" app.



### Step 2.

Open the 'Required args' section and indicate the directory containing the FASTA files you wish to analyze. You also need to include an accessions mapping file. Samples can be found in directory '/iplant/home/shared/imicrobe/16sblaster' which can be found by choosing the 'Data' button on the left, then going to 'Community Data -> imicrobe -> 16sblaster'.

16sblaster

Analysis Name: 16sblaster\_analysis1

\* Required args

Input directory (FASTA):

Select a folder Browse

\* Accessions map file:

Select a file Browse

\* Output directory name:

16sblaster-out

Options

Launch Analysis

You can use the 'Options' to change the default values for similarity, etc.

16sblaster

Analysis Name: 16sblaster\_analysis1

\* Required args

Options

Similarity:

0.98

Percent of total reads:

0.01

Length:

25

Species hit:

98

☐ Verbose

Launch Analysis

Click on the 'Launch Analysis' button and await an email notification of the job's ending status.

### Step 3.

In the output directory (default "16sblaster-out"), you will find a large number of files used in the analysis. The "ALL\_RESULTS.txt" and "SUMMARY.txt" files will be of interest to you.

