# PUMA with Agilent arrays

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Open the Tiff-splitter program from the Agilent directory in the start menu.
Split all the arrays.
Using SFTP, upload the following files for each array into your incoming directory on loader: red tiff, green tiff, shp file, txt file

## Database

Log in to the database. Under Enter Data, click Experiments and Results.
Click Enter a New Experiment into the Database.
Select Agilent, Agilent, and Saccharomyces cerevisiae from the 3 pulldown menus. Click Enter a New Experiment.
Fill out the experiment description form. Choose the print from the menu. Make sure all the files match. Pick a logical category and subcategory. If the reference was in the red channel, click the dye swap box. Select your collaborators from the list to give them access. Put in as much information as possible. You will probably not go back and add in extra documentation later. Do it now.
Submit the form to the database.
You will get an email confirming that the files have been submitted to the database, then another one when they have been actually placed in the database. Go to the URL in the second email and look at the submission data. Make sure everything looks OK.

To look at the data, go to the search section, select any subcategory or user filters, and hit data retrieval and analysis.
Select the experiments you want to analyze from the list.
Choose Data Retrieval and Analysis.

I typically retrieve data by SUID, which averages all the spots that are for the same gene, as long as they pass your filters. On occasion, you may want to retrieve by spot to make sure your replicates are actually correlating.
Select any biological annotations you want.
Choose what label you want on each experiment.
Proceed to Data Filtering.
I usually retrieve the Log (base2)(REDsignal/GREENsignal).
Invert any dye swaps.
Choose your filtering criteria. I usually just use significantly above background in either channel (i.e., 1 OR 2)

If you would like to actually inspect the spots, click the box next to retrieve spot coordinates.
Download the resulting .pcl file, or proceed to filtering/clustering as desired.  Or add it to your repository.