

Data Retrieval

We are now using the Geospiza Finch-Server as a web-based interface for retrieving sequencing data. RTSF will upload completed custom sequencing results (chromatograms and bases/reads) from the Applied Biosystems (ABI) Sequencer to the Finch-Server database. The sequencing data are processed automatically and quality values are assigned using the phred algorithm.

Navigating the Finch Server Website

- The “Welcome Page” contains a menu on the left side to aid in navigation.
- Click on the “Finch Icon” (upper left corner of the title bar) to return to the “Welcome Page” from any location.
- From the “Welcome Page”, click on “Documentation” to launch the online user manual. This manual is also available by clicking on the “i” button in the upper right corner of the title bar.
- Where appropriate, links are indicated in “blue” and additional links are underscored.
- The “Sequencing Request” section in the “Welcome Page” is not operational and should not be used.
- We request that you do NOT “Add Folders”.

Retrieval of Sequencing Results

- Sequencing results are retrieved with your web browser. In order to perform properly with Finch-Server, the browser software must be configured to use JavaScript. Most popular browsers are configured to use JavaScript by default. If your browser does not support JavaScript, we recommend updating to the latest version of your favorite browser.
- Connect to the Finch-Server by logging in to <http://finch.bch.msu.edu/> (Bookmark this location for future reference). First time users, please consult Logging in for the first time
- To see your Finch-Server folder, which contains all sequence results for the entire lab, do the following:
 - From the “Welcome Page”, under the “Reports” section, click on the “Folders” link.
 - From there, click on your “Folder Name” (your lab initials). Clicking on your folder name shows details of the entire folder, including a phred Q20 histogram. This histogram summarizes all of your laboratories’ custom sequencing submissions.
- To get to data for a single clone:
 - From your folder (see step 3) click on “Reads in Folder” and then the desired Clone ID. This will display the chromatogram details; the phred quality values for each base, indicating total read length, trimmed length and Q20 length; and the phred sequence with quality trimmed regions and vector regions identified. You may “view trace” (i.e., view the phred-based called chromatogram) and print this view if you desire; and “export”; (the “view contents” feature is not active).
 - You may also “export” the sequence and/or the chromatogram. This allows you to save the data for a given sequence to your personal computer. See Exporting sequences and chromatograms for details.
 - RTSF will continue to print ABI-based called chromatograms for all custom sequencing submissions. As usual, the chromatograms will be inserted in the sequencing folders and may be picked up outside Room S18, Plant Biology Building. Starting Nov 1/01, laboratories/individuals NOT requesting RTSF-printed chromatograms will experience a \$0.50 reduction in cost.

- For specific questions relating to computer setup and operation, including installing programs to manipulate sequence data, we suggest you contact your departmental computer specialist as they will have the most information about your particular system.