

MICROMON SANGER SEQUENCING

ACCESSING YOUR DATA FILES FROM THE MICROMON FTP SERVER

When your data is available for download from our server, we will send to you an e-mail notification message with the subject header 'Micromon Sanger Sequencing'. Results will be cleared from the server when they become 14 days old. Don't panic if you missed downloading your files because we keep permanent archived copies of all data and can upload them again on request.

ACCESSING YOUR DNA SEQUENCING DATA USING A WEB BROWSER

Insert our server IP Host Address **130.194.155.49** in the address box for your browser and hit Return. The Micromon Genomics login window will mount. Alternatively, you can login via the access button on our webpage, or the link that is shown in the signature of our notification emails.

There are two download options:

1. Download your entire folder in Zip format (use the download arrow at far right when in folder view). This is the desirable option if you have numerous data files.
2. Open your folder and download each file individually.

ACCESSING YOUR DNA SEQUENCING DATA USING AN FTP CLIENT PROGRAM

FTP ACCESS SOFTWARE

The FTP client program **FileZilla** is one of the most commonly used and is freely available for both Windows and Mac systems. These programs are simple and user-friendly, and allow the consecutive transfer of multiple files to a local directory with a single command action.

A freeware version of FileZilla can be downloaded from the [FileZilla Project website](#)

Once installed, you will need to enter our **IP Host address** in the address box

130.194.155.49

Then type your allocated username and password into the relevant boxes. These parameters can be permanently set in FileZilla using the 'Site Manager' tool.

Once you have downloaded the electropherogram (.ab1 file) to your local computer, an [electropherogram viewing program](#) is required to open this type of trace file. The viewing software will allow you edit the entire sequence data run plus generate prints on your own black and white, or colour printer if desired.

It is critical that you view the electropherogram (trace file) for the full length of the read to perform the manual editing check. Where the data is poor, the Kb basecaller will occasionally make an error where it determines that the base spacing is irregular or the resolution of the peaks is too low (nearer the end of the run).