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Author: F. Yalcin, Wellcome Trust Sanger Institute, Hinxton, U.K.

E-mail: fy2@sanger.ac.uk

Description: Please follow the steps in this file to access your PAGe data.

1. Connect to the Sanger FTP server with FileZilla

Connect to the Sanger FTP server with an FTP client.

In this document we describe the connection with the "FileZilla client" (Download and install the client from: http://filezilla-project.org/).

To establish a connection to the Sanger FTP server with the FileZilla FTP client, follow the four steps below:

- 1. Enter "sftp://sftpsrv.sanger.ac.uk" into the host field of the Quickconnect bar in FileZilla (see Figure 1).
- 2. Enter your assigned "FTP username" and "FTP password" in the corresponding fields (This will be sent to you in a private email).
- 3. Leave the "Port" empty.
- 4. Click on "Quickconnect" or press Enter to connect to the Sanger FTP server.



Figure 1: FileZilla Quickconnect bar

2. Download the files to your local machine

After a successful connection attempt, a list of files and directories appears on the right side of the main window. The name of the current remote directory is listed in the edit field on the top. Below that you will see the remote directory tree. Under the remote directory is a list of the contents of the current remote directory.

First change the current remote directory to your "FTP data directory" (This will be sent to you in a private email) then download its contents, i.e.:

- 1. Double-click your "FTP data directory" in the list of the current directory contents.
- 2. You should see three files ("README.txt", "annotation.tar.gz" and "name.mapping.txt")
- 3. You can upload or download a file by double-clicking on it. It will be added to the transfer queue and the transfer starts automatically. To transfer directories and/or multiple files, select them and right-click the selection. Then you can click on Upload/Download in the popup menu.

3. De-compress the "annotation.tar.gz" file

The annotation.tar.gz is a compressed archive file. Run the following command in a unix operating system terminal in order to de-compress this file:

tar -xzvf annotation.tar.gz

The command above should create a directory called "annotation" with one EMBL file per isolate. See the README.txt file for more details.