

Instructions to create a publicly accessible weblink to read genomic data from Northwestern Quest onto the UCSC Genome Browser tool

Apply for a Quest allocation

Quest is Northwestern's high performance computing cluster. Northwestern members are provided free access to Quest resources through an allocation process. **Note – Legally and contractually restricted data, such as data subject to HIPAA and FISMA, should not be stored on Quest.**

Apply for an allocation at <https://www.it.northwestern.edu/departments/it-services-support/research/computing/quest/general-access-allocation-types.html>

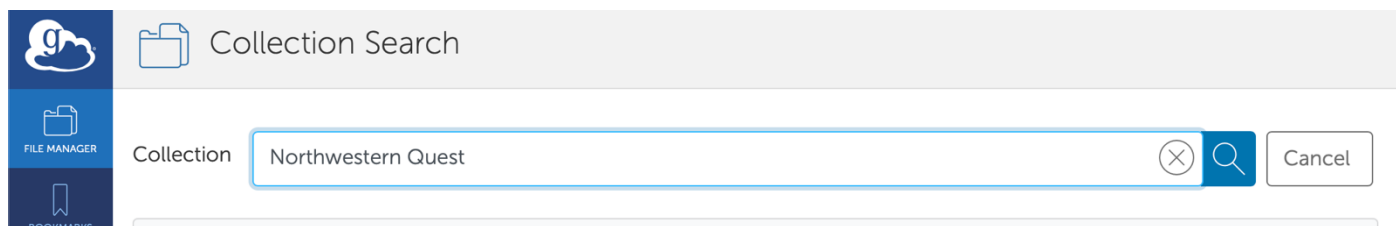
Install Globus Connect Personal on your machine

Globus is a data transfer tool that allows for easy file-sharing between two endpoints. Globus refers to the places that data are stored (such as your computer, Quest, RDSS, the cloud) as endpoints. **Note – Globus should not be used to transfer legally and contractually restricted data, such as data subject to HIPAA and FISMA.**

Go to <https://www.globus.org/globus-connect-personal> and install Globus Connect Personal, a desktop app, on your local machine. Login to Globus with your Northwestern credentials.

Access the Northwestern Quest endpoint on Globus

1. Login to Globus through the website (<https://www.globus.org/globus-connect-personal>)
2. Navigate to the Globus **File Manager** tab on the left sidebar
3. Click inside the **Collection** search bar and type in “Northwestern Quest” as shown below



4. Navigate to the Northwestern Quest endpoint shown below (owner northwestern@globusid.org) and click to authenticate your credentials. There are several endpoints named “Northwestern Quest” so be careful to choose the one shown below.



Northwestern Quest

Managed Mapped Collection (GCS) on Northwestern Quest - qglobus11

Owner: northwestern@globusid.org

Domain: m-b55e05.a0115.5898.data.globus.org

Description: Endpoint provides the access to the HPC Quest cluster for big data transfers.



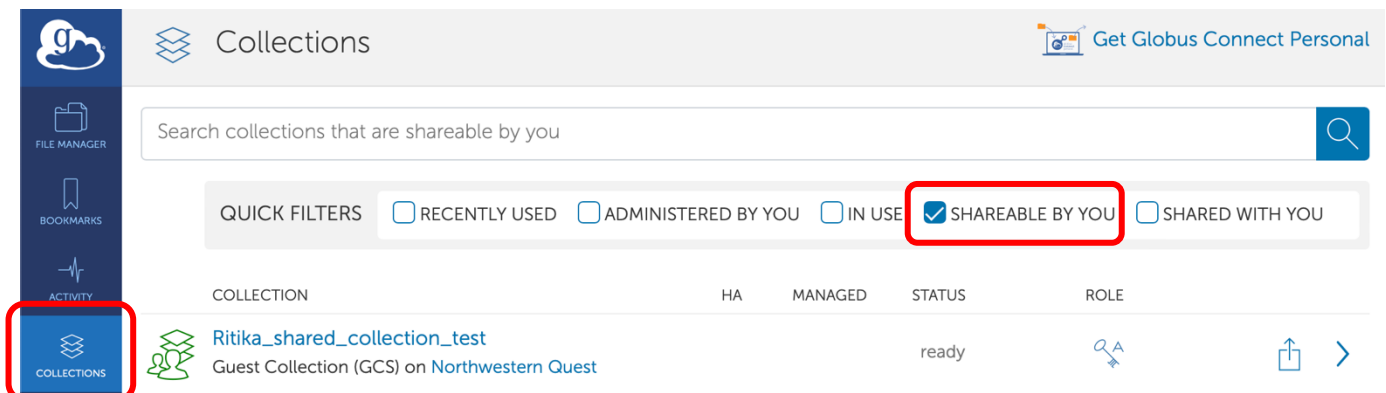
Create a shared collection and set permissions to public

Your collaborators, especially those outside of Northwestern University, may not have access to all of the locations that you store your data, including data on Northwestern managed endpoints. Globus allows you to grant read and/or write access to collections to any Globus user, even if they do not have a Northwestern NetID. Additionally, you can create shared collections on managed endpoints to avoid having to reauthenticate after the activation expires.

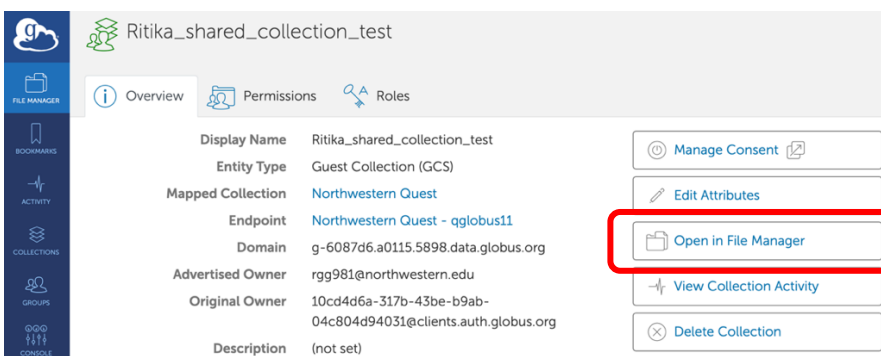
1. Create a **new** folder which will become your shared collection folder. Place **copies** of your **genomic data files** in this newly created folder. Name this folder with a unique identifier ideally prefixed with your NetID. For example: *abc234_mouse_olfactory_data*. This will help you to easily locate your shared collection endpoint whenever required. The advantage of creating a new folder is that once you are done visualizing, the shared files and associated public URLs can be safely deleted without losing your original data files.
2. In order to create a publicly accessible shared/guest collection using this new folder, follow the instructions at <https://docs.globus.org/how-to/share-files/>
3. **Set the Share Permissions to Public and read only** – this will allow an external application like UCSC Genome Browser to read the data in this folder. Note that anyone with this link will be able to access this data.

Get a public weblink for your file

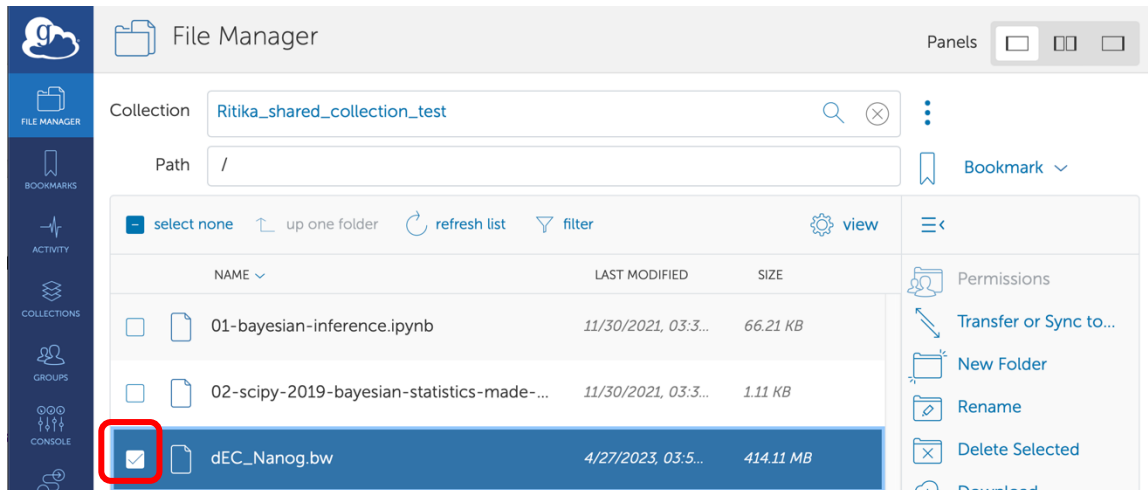
1. Login to Globus at <https://www.globus.org/globus-connect-personal>
2. Navigate to **Collections** tab on the lefthand sidebar
3. Click on **Shareable by you** to bring up a list of your shared collections
4. Click on the shared collection to open the overview



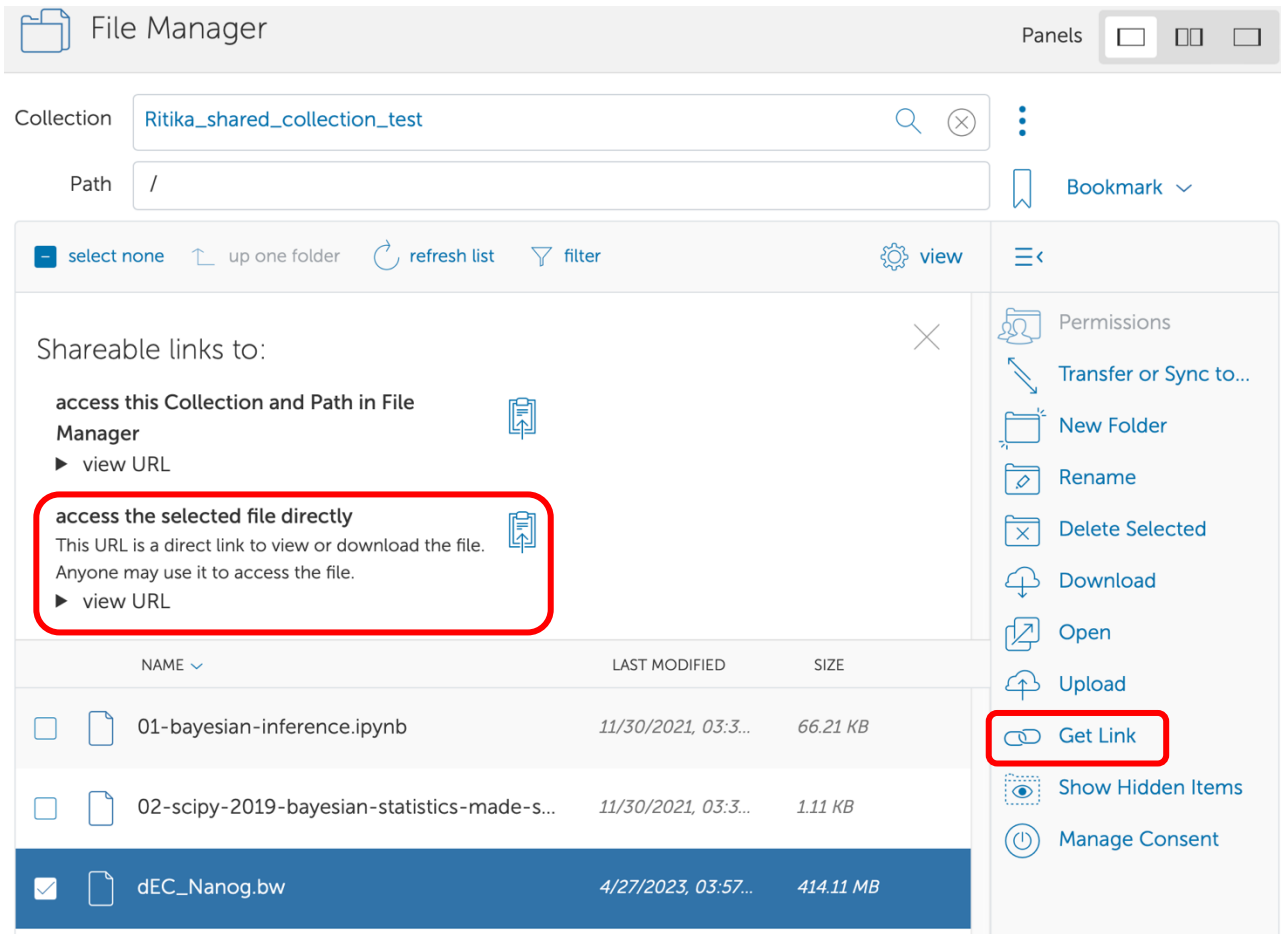
5. Inside Overview, click on the **Open in File manager** option on the righthand side.



6. Inside File Manager, click the checkbox to select the data file you want to visualize.



7. Now select **Get Link** from the right-hand side options panel. You will now see 2 shareable links for the selected file as shown below.



8. Copy the URL titled “**access the selected file directly**” using the copy icon next to the link. This is a publicly accessible URL for your genomic data file. Paste this URL in the UCSC Genome Browser custom tracks tool to view your data on the Genome Browser web application. Once the shared file or collection folder is deleted, the public link will no longer work. Please ensure that you are working with file copies so as not to lose the original data.