


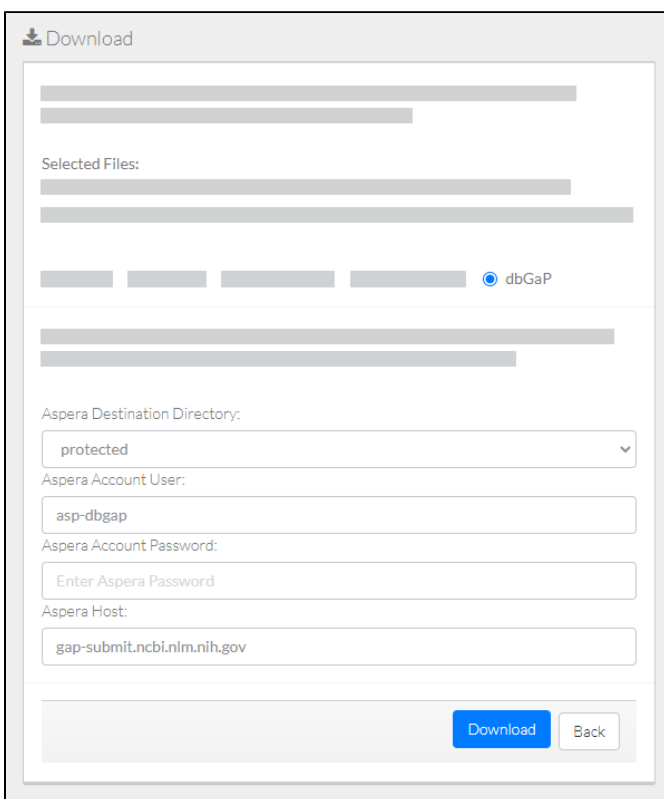
Submitting to the NIH dbGaP via the GUI

If your user account has the Read permission level on data in DME, you can transfer that data from DME to [dbGaP](#).

1. Log in as described in [Logging In via the GUI](#). The Dashboard appears.
2. Select data for transfer, using one of the following options:
 - Browse for the data, as described in [Browsing for Data via the GUI](#). The top of the detail panel displays the size of the selected collection.
 - Search for the data, as described in [Searching for Data via the GUI](#) (or run a saved search from the Dashboard). The search results page appears. In the selection column, select each item you want to transfer. When performing a *detailed* search, the total size (of selected collections or data files) appears above the table.
3. Initiate the download:
 - In the search results page, click the download icon () above the list.
 - In the Browse page detail panel, in the row for the collection or file you want to download, click the download icon.

The Download page appears.

4. Select **dbGaP**.



5. Specify Aspera information:

- Destination directory
- Account password

Keep the default account user name and host name.

6. Click **Download**. The system responds as follows:

- The system begins to transfer the data based on your selections and displays the task ID link.

To view the progress of this transfer, click that link. The Collection Download or Data Object Download Task Details page appears. For instructions, refer to [Viewing the Details of a Download Task](#).

- Depending on your event subscriptions, the system might send you an email notification of the transfer status. For instructions on subscribing, refer to [Subscribing to Download and Registration Notifications](#).

If you experience any download failures, contact NCIDataVault@mail.nih.gov.