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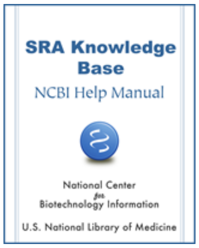

Downloading and Accessing Data

Sequence Read Archive Submissions Staff

Created: August 22, 2011; Updated: March 18, 2014.

This section of the Sequence Read Archive (SRA) Knowledge Base contains:

- Instructions for downloading data from the SRA website
- Instructions for downloading data using command line utilities
- Instructions for downloading SRA data from dbGaP**
- Information for dealing with problems that may arise during the download process
- Information on converting .sra files into other formats and direct downloads of fasta and fastq format data

** **Please Note**: The information provided in this section regarding the download of individual-level data from dbGaP assumes that you have completed the dbGaP data access request process, and have been granted authorized access to individual level data.

If you do not have authorized access to dbGaP individual-level data, you will not be able to access individual-level data using the instructions in this section, since you will not have access to the appropriate password-protected dbGaP sites mentioned. For information on how to apply for authorized access, please see the "Data Access Request" section of the dbGaP FAQ Archive.

To begin searching this section of the Sequence Read Archive Quick Start, you can:

- **Enter** your **search word(s)** text in the text box **at the top of the page** and click on the "Go" button

  OR
- **Clickon** any of the "GenBank Submission Resources Quick Start" **sub-categories listed** in the "Contents" section **below** to go to the sub-category of your choice.