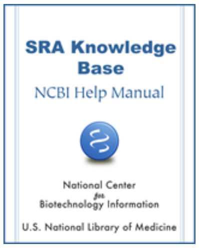
U.S. National Library of Medicine
National Center for Biotechnology Information

NLM Citation: Sequence Read Archive Submissions Staff. Searching for Species-Specific Data. In: SRA Knowledge Base [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2011-.
Bookshelf URL: https://www.ncbi.nlm.nih.gov/books/


SRA Knowledge Base
NCBI Help Manual
National Center for Biotechnology Information
U.S. National Library of Medicine

Searching for Species-Specific Data

Sequence Read Archive Submissions Staff

How do I find SRA data for African strains of fruit fly using Entrez SRA?

Enter the search phrase **fruit fly AND Africa** or **Drosophila AND Africa** into the Entrez SRA search box, and click the "search" button.

- You can make your search more specific by using Entrez search limits. Click the "Limit" link to specify a value for any or all of the following:
  - Publication date
  - Search Field Tags
  - Access level
  - Date Modified
  - Molecule
  - Availability of loadable data

Once you have specified your limits, click the "Search" button on the Limit page to apply your limits to the search terms you entered in the search box at the top of the page.

- You can also make your search more specific by using the Entrez "Advanced" search. Click the "Advanced" link to go to the SRA Advanced Search page, which contains:
  - "Search Builder"
    This tool helps you select search fields and field values to create a search statement that reflects your specific search requirements.
  - "Search History"
    This tool keeps a record of up to 100 searches and their results so that you do not duplicate searches and can combine previous searches for more specificity.
- For help using Entrez "Limits" or "Advanced" search options, see the Entrez Help documentation.

Note: Since SRA is a raw data archive (not curated) and can index only those terms that a submitter provides in the metadata of their submission, your search results may not include all possible studies associated with your search term.

How do I find SRA data for African strains of fruit fly using the "Object Search" tab on the SRA home page?

Enter the search phrase **fruit fly AND Africa** or **Drosophila AND Africa** into the "Search for SRA related objects" search box, and click the "search" button. You can use any Entrez search statement in SRA's "Search for related objects", but this search page does not have the "Limit" and "Advanced" search features that the Entrez SRA search has.

Note: Since SRA is a raw data archive (not curated) and can index only those terms that a submitter provides in the metadata of their submission, your search results may not include all possible studies associated with your search term.

How do I find SRA entries for sequenced complete genomes of the Euryarchaeota group of archaea?

1. Go to the Entrez Taxonomy page.
2. Enter **Euryarchaeota[organism] AND taxonomy_sra[filter]** in the search box at the top of the page.
3. Click the “Search” button.
4. The response page provides you with a list of the organisms in this phylum that have published SRA sequencing.
5. Click the organism of interest to go to the Taxonomy Browser page for that organism.
6. Click on the link for “SRA Experiments” under “Entrez Records” for this organism to go to the SRA database.
7. You will see a list of experiments (SRX/ERX/DRX accessions).
8. Click on the SRX record of interest. The record will include:
    a. Links to each run in the experiment
    b. Experiment design information
    c. Submission accession and submitter name
    d. Study summary and abstract (if available)
    e. Experiment sample (SRS) information
    f. Links to a list of experiments (SRX)
    g. Library information (if available)
    h. Platform information
    i. Processing information (base calls and quality scores)
    j. Spot descriptor information
    k. Links to related information
9. At this point, you can do one of the following:
    a. **Click on the “All experiments” link** for a complete list of the experiments included in the study.
    b. **Download the data for a particular experiment** by clicking on the SRA or the SRA-lite download links. These links will take you to the SRA FTP site where the files are available for download. If there are no download links in the experiment record, please contact sra@ncbi.nlm.nih.gov.
    c. **Click on one of therun links(**SRR/ERR/DRR**accessions)** to go to the SRA Run Browser, where you can look at individual reads, search the spots for a specific sequence, or download a set of spots from the run.

Note: Since SRA is a raw data archive (not curated) and can index only those terms that a submitter provides in the metadata of their submission, your search results may not include all possible studies associated with your search term.

Note: If you choose to download files, install the “Aspera Connect” plug-in to transfer files at a significantly faster rate than ftp.