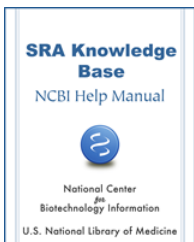




U.S. National Library of Medicine  
National Center for Biotechnology Information

**NLM Citation:** Sequence Read Archive Submissions Staff. Searching for Data Referenced in a Publication. In: SRA Knowledge Base [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2011-.

**Bookshelf URL:** <https://www.ncbi.nlm.nih.gov/books/>



## Searching for Data Referenced in a Publication

Sequence Read Archive Submissions Staff

**The paper I'm reading says all the data described in it was deposited in SRA, but it doesn't list any accession numbers. How do I find the data?**

There are many reasons that accessions may be unavailable (e.g. the submission may be incomplete or the submission may be released but not indexed). If the paper you are reading mentions that the data was submitted to SRA, but does not provide accession numbers for the data, please contact [sra@ncbi.nlm.nih.gov](mailto:sra@ncbi.nlm.nih.gov).

**There are SRA accession numbers in the PubMed article I'm reading, but there are no links to SRA from the accessions.**

We must create a link *from SRA to the accession* in a PubMed article. If you find a PubMed article containing SRA accessions that do not have links to SRA, please contact [sra@ncbi.nlm.nih.gov](mailto:sra@ncbi.nlm.nih.gov), and we'll insert the links.

## Unable to Find Data in SRA Using ID given in Publication

**When I search for a submission accession (SRA) provided in a publication, I get a list of accessions for experiments (SRX) rather than the actual submission. How do I get data for a submission accession (SRA)?**

An SRA submission accession number does not represent a single *object* the way a GenBank accession number represents a single object (a sequence) submitted to GenBank. The SRA submission accession is an artificial packaging construct that groups together a number of objects, and therefore has no specific response page.

For example, the GenBank accession [NM\\_001048036.2](#) represents a single object: a GenBank sequence submission (in this case, a RefSeq mRNA from the domestic dog). An SRA (submission) accession number (e.g. [SRA010122](#)), doesn't represent a single object – it is a reference number that represents a group of objects that includes all of the following:

**Study** (a metadata object that describes the entirety of a sequencing study — these are represented by SRP/ERP/DRP accession numbers) .The study accession housed by submission SRA01012 is [SRP001451](#).

**Experiments** (metadata objects that describes the experiments within the study — these are represented by SRX/ERX/DRX accession numbers). One of the experiment accessions contained in SRA010122 is [SRX013300](#)

**Runs** (objects containing sequencing run data files and their associated metadata— these are represented by SRR/ERR/DRR accession numbers) One of the run accessions contained in SRA010122 is [SRR030732](#)

**Samples** (metadata objects that describe material sequenced in the study — these are represented by SRS/ERS/DRS accession numbers). One of the run accessions contained in SRA010122 is [SRS007212](#)

**Analysis** (a packaging construct for data objects [and their associated metadata] generated by different types of sequence analysis: e.g. assemblies, alignments, etc.)

Because a submission accession (SRA) is not an object itself but a [container](#) for objects (SRP, SRX, SRR, etc.), when you search for a particular SRA accession, you will get is a list of the experiments (SRX accessions) from the submitted study. The experiment entries contains links that will take you to the all the other objects contained in a particular submission.

In time, we hope to generate a response page specific to submission (SRA) accession searches. This response page will contain links to all the objects contained by the submission accession.