



## Searching using BLAST

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### Can I conduct a sequence similarity search (BLAST) against data in the SRA?

Yes you can. NCBI offers a nucleotide BLAST service for [sequence similarity searches of SRA transcript and genomic libraries](#). You can access this service using one of the following routes:

- Go to the [BLAST home page](#), and select the “Search SRA transcript and genomic libraries” link located in the “Specialized BLAST” section
- Go to the [SRA home page](#), click the “Search” tab, select the “BLAST” link, and when you see the [response page](#), select the “Search transcripts” link to get to the BLAST SRA page.

**Note:** Currently, BLAST only works with data sets that have long sequence reads. This means that an SRA BLAST search will not work with any data sets that may have been submitted for a species that have short sequence reads.

If you require a sequence similarity search against species data that is in the SRA but is not listed as available for BLAST, SRA does offer a limited sequence similarity search for a subset of spots within a run. Go to the [run browser page](#) for a run of interest and enter your sequence in the “Filter” text box and click the “Find” button. You can also search for spots within a run using:

- The name of the spot
- OR
- The sample pool member

### I would like to BLAST my sequence against SRA, but I don't see the species I would like to BLAST against listed in the search set menu.

Because a successful BLAST search requires reads longer than some SRA data sets contain, not all SRA submissions can be used for a BLAST search.

If the species that you are interested in BLASTing against isn't in the SRA BLAST list, then it means that data with long enough reads to be useful for BLAST has not been submitted for it yet.

**If you require a sequence similarity search against a species data that is in the SRA but is not listed as available for BLAST, SRA does offer a limited sequence similarity search for a subset of spots within a run.** Go to the [run browser page](#) for a run of interest and enter your sequence in the “Filter” text box and click the “Find” button. You can also search for spots within a run using:

- The name of the spot
- OR
- The sample pool member