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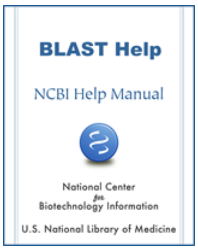
NLM Citation: BLAST® Command Line Applications User Manual [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2008-. Faster sequence lookups by accession. 2008 Jun 23 [Updated 2021 Jan 7].
Bookshelf URL: https://www.ncbi.nlm.nih.gov/books/



Faster sequence lookups by accession

Created: June 23, 2008; Updated: January 7, 2021.

Starting with BLASTDB version 5, blastdbcmd has two additional parameters (-taxids and -taxidlists) to efficiently retrieve sequences by taxid.

```
# Retrieves all human entries;
# %a prints the accession, %T prints the taxid, %S prints the scientific name
$ blastdbcmd -db nr -taxids 9606 -outfmt “%a %T %S” -target_only
```

Note: -target_only is used to ensure that only accessions for the human entries are present. Otherwise, it will present all accessions on any sequence with at least one human sequence. This is important since nr is a non-redundant database.