



## Faster sequence lookups by accession

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.