# How To: Download all the reference sequences for a set of proteins (e.g., all *aac(6')-lb* sequences)

**NCBI** Pathogen Detection

https://www.ncbi.nlm.nih.gov/pathogens



U.S. National Library of Medicine National Center for Biotechnology Information How do I download all the reference sequences for a set of proteins? (e.g., all *aac(6')-lb* sequences)

- Use <u>MicroBIGG-E</u>
- Use filters or search to select gene family "aac(6')-lb\*"
- Download table containing protein accessions
- Use Batch Entrez to download proteins



#### https://www.ncbi.nlm.nih.gov/pathogens

### Pathogen Detection **BETA**

To assist the National Database of Antibiotic Resistant Organisms (NDARO), NCBI Pathogen Detection identifies the antimicrobial resistance, stress response, and virulence genes found in bacterial genomic sequences. This enables scientists to track the spread of resistance genes and to understand the relationships between antimicrobial resistance and virulence.

NCBI Pathogen Detection integrates bacterial pathogen genomic sequences originating in food, environmental sources, and patients. It quickly clusters and identifies related sequences to uncover potential food contamination sources, helping public health scientists investigate foodborne disease outbreaks.

There has been a change to the *Isolation type / epi\_type* attribute that affects *min-same/min-diff* computation. Now where an isolate has no information to support the setting *environmental/other* the Browser will no longer default to that value but instead present as *NULL*. This means that the *min-same/min-diff* values for this isolate will present as *n/a*, and other *min-same/min-diff* values for isolates clustered with this isolate may change. Please see the <u>Help</u> text for more details.

#### Learn More About FAQ **Browser Factsheet** Antimicrobial Resistance Factsheet Antimicrobial Resistance Contributors Help Data Resour 1. Click Reference **Gene Catalog Isolates Browser** Microbial Browse Genomic Elements (Mi G-E) **Reference Gene Catalog** NEW Reference HMM Catalog

#### <u>Health</u> > <u>Pathogen Detection</u> > Reference Gene Catalog

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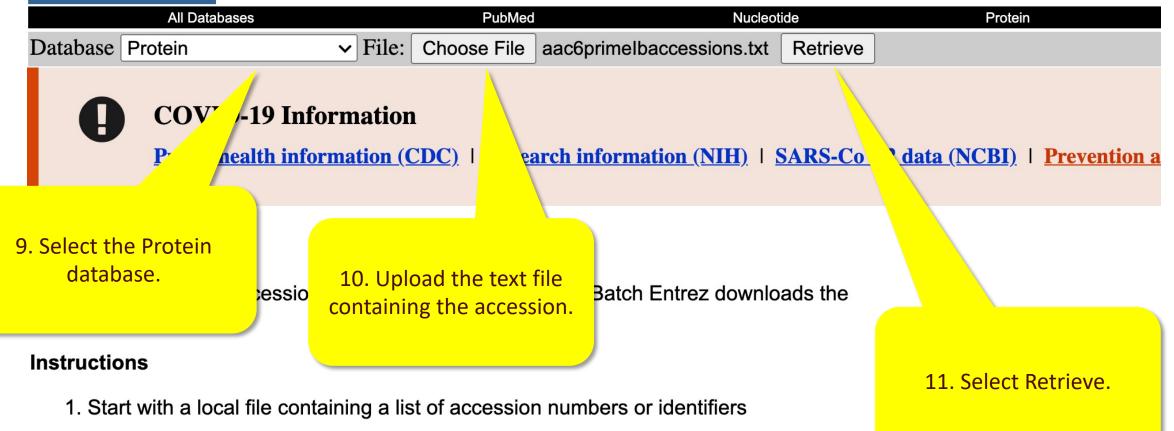
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8. Place the protein accessions into a single column text file, with one accession per row. Then go to Batch Entrez

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### **Batch Entrez**

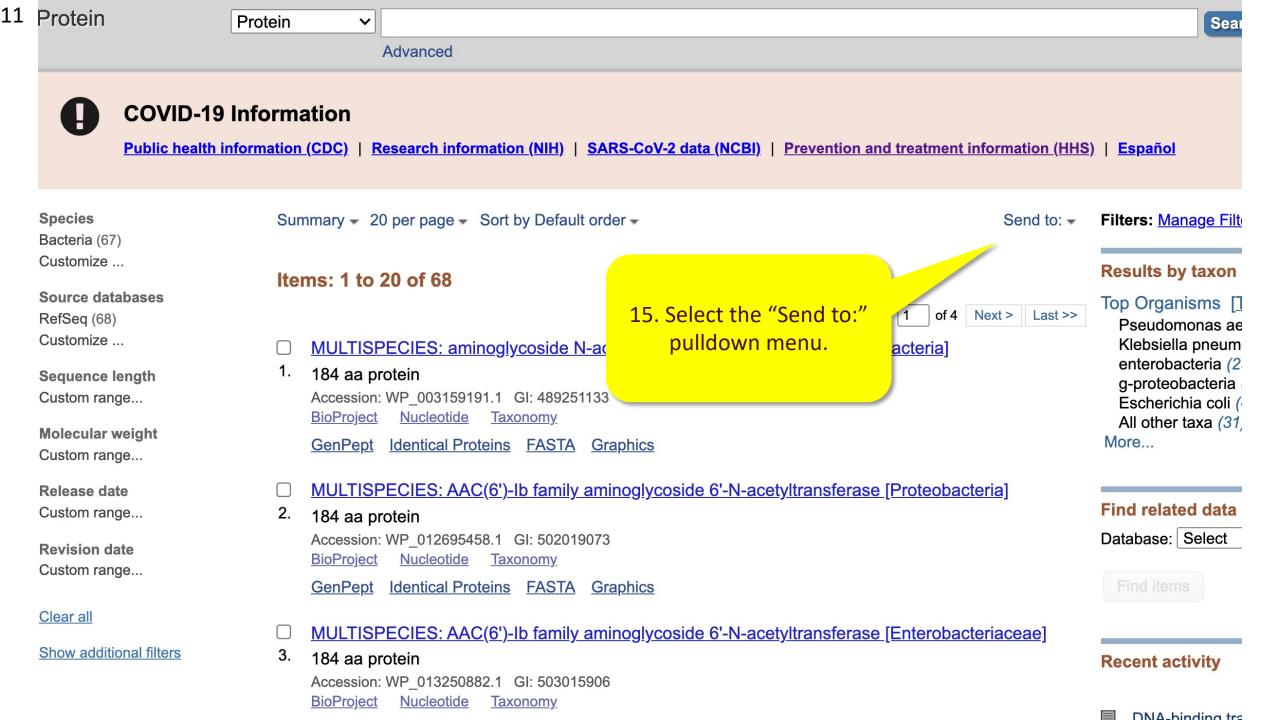


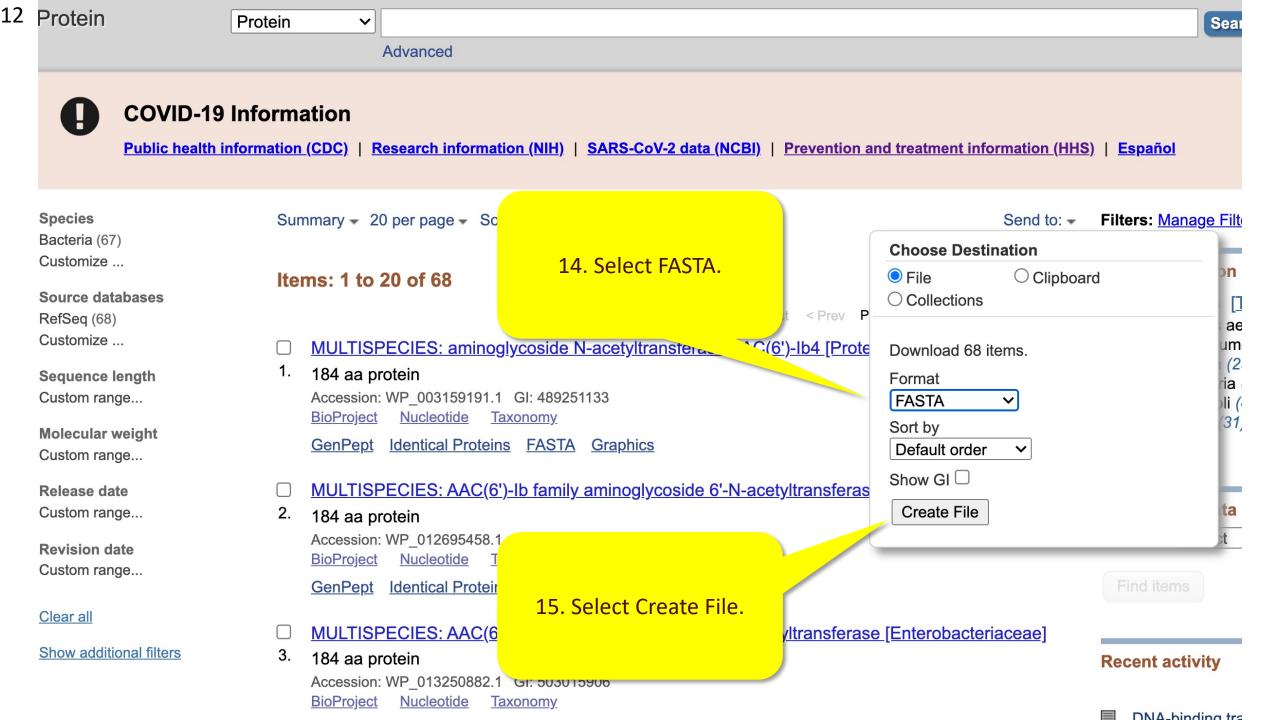
- 2. Select the database corresponding to the type of accession numbers or identifiers in your input file
- 3. Use the Browse or Choose File... button to select the input file
- 4. Press the Retrieve button to see a list of document summaries
- 5. Select a format in which to display the data for viewing, and/or saving
- 6. Select 'Send to file' to save the file.

10

Received lines: 68 Rejected lines: 0 Removed duplicates: 0 Passed to Entrez: 68 <u>Retrieve records for 68 UID(s)</u>

12. Select Retrieve.





## More information

- For full help documentation of the Reference Gene Catalog see: <a href="https://www.ncbi.nlm.nih.gov/pathogens/pathogens\_help/#reference-gene-catalog">https://www.ncbi.nlm.nih.gov/pathogens/pathogens\_help/#reference-gene-catalog</a>
- For details about filters see: https://www.ncbi.nlm.nih.gov/pathogens/pathogens\_help/#refgene-filters
- For details about the table downloads see: https://www.ncbi.nlm.nih.gov/pathogens/pathogens\_help/#refgene-access-download

Questions and further help: email pd-help@ncbi.nlm.nih.gov

