

Sequence-ID

Choose a tab to identify species using BLAST against a curated database

Blast

[Help](#) ▾

blastn search

Job name

Input FASTA format
sequence here:

```
>Query file
GTGAGTACCTTGGGCTGCCTTTATATATAATCTAGAAACAAGGCCCTT
TAAGGCCCTTTCCTCCTCCTCCCAAAGCTATAAAAGATATTTGGGT
GAATTCACAGCTTCAGGCTATGGAACCTCTGGATTCCCTCCTCCAC
TCCACCCTACTGCAGAGATGCTGAGAAAGTCTGGGAGGGTTTTCTA
AAAGCTAAGCTGGGCCAAATAGCCAGGTTCAAGTCAGTACATGAAGA
GTTGTGGTTCTAAATTCCTTCCCTACTCCAGCTCCAAATTTCAATTTAG
TTCCACTTTTGGGCCTAACCCAGCTAAAGGTCCCCACCCAGCTCCTG
CTATCTAGTCACTGCATATGGCAGACCTTGAAAGTCCATCTCAAAGC
AGCAGAATTATCAGTTATCTGTCTTGTGCATGGAAAAGAGAGATAAGCA
AGGCCTGAGAAAGGAGTCTGGAGCTCCAGCTTCTGGTACACATCCT
```

Submit and run

Supplementary Figure 1. Screen capture of the Sequence-ID user interface of Microbe-ID. The interface includes tabs for input of barcodes and a dropdown help link that contains laboratory protocols, examples data, and logs of each query dataset. The input frame has a control scheme that only permits data in FASTA format.