**Uploading BLiMMP metatranscriptomes to NCBI**

All raw metatranscriptomic data from this study will be made available through NCBI. This document outlines how I uploaded the data to NCBI. These metatranscriptomes will be linked to the BioProject and BioSamples generated for the metagenomes. The details on how I prepared those can be found here: `code/metagenomes/metagenome\_upload\_to\_NCBI.docx`.

Log in to NCBI using ORCID

**Step 1:** Upload raw (untrimmed, unassembled) metatranscriptomes to the Sequence Read Archive (SRA).

1. <https://submit.ncbi.nlm.nih.gov/subs/sra/>
2. We’ll upload using the “FTP upload options”.
3. **Navigate to the source folder** where the files for submission are
   1. **Navigate to folder: `cd ~/BLiMMP/dataRaw/**metatranscriptomes**`**
4. **Set up screen: `screen -S BLiMMP\_MT\_upload`**
5. **Establish an FTP connection** using the credentials below:
   1. Address: ftp ftp-private.ncbi.nlm.nih.gov
   2. Username: subftp
   3. Password: w4pYB9VQ
6. **Navigate to your account folder**: cd uploads/petersonben50\_gmail.com\_2kD7rlpc
7. **Create a subfolder (required!)** with a meaningful name: mkdir BLI\_data\_MT
8. **Navigate to the target folder** you just created: cd BLI\_data\_MT
9. **Copy your files into the target folder**:
   1. Prompt
   2. mput \*
10. After the FTP has finished, go back to <https://submit.ncbi.nlm.nih.gov/subs/sra/> and click on New Submission
11. Submitting this with my UW-Madison info.
12. General Info
    1. Provide the BioProject ID (PRJNA876614)
    2. Did already register BioSample IDs
    3. Set release date to 2023-10-01
13. SRA Metadata:
    1. Batch upload. Excel sheet is here: dataRaw/metatranscriptomes/ NCBI\_SRA\_metadata\_acc.xlsx. Back to code/metagenomes/metagenome\_metadata.R to prep the data. Save out to “dataRaw/metatranscriptomes/temp\_NCBI\_info\_SRA.csv”, then add data to xlsx file.
14. Files: “FTP or Aspera Command Line file preload”
    1. Select the BLI\_data\_MG folder.
15. Review and confirm.