Tess Brewer, PhD

Email: tess.brewer@eawag.ch *Github*: github.com/tessbrewer *Languages:* English (native)
Publication list: Google scholar profile *OrcID*: 0000-0001-7855-5610 German (B1)

I'm a Zurich-based microbiologist applying both computational and experimental approaches to investigate diverse bacteria. With expertise in bioinformatics, statistics, molecular biology, and protein biochemistry, I contribute across the full research cycle, from data generation to advanced analysis.

Skills

Laboratory: Aseptic technique, protein purification, heterologous expression, cloning/plasmid design, PCR, qPCR, DNA/RNA extraction, prep & optimization for NGS sequencing

Bioinformatics: Amplicon & metagenomic-based sequence processing/analysis (long & short read), genome assembly (isolate & metagenomics-based), SNP analysis, ribosomal profiling analysis, data visualization & phylogenetic tree based-analyses, comparative genomics, phylogenetic-based statistical methods

Computational: R***, Terminal/Bash**, Linux**, Python**, Shiny*, Git version control*, Nextflow*
Advanced (***), Intermediate (**), Familiar (*)

Education

Ph.D. Molecular, Cellular, and Developmental Biology — University of Colorado Boulder (USA)
2013 – 2019, Advisor: Noah Fierer

Dual B.S. Biochemistry & Biology with Honors — Florida State University (USA)
2008 – 2012, Advisor: Kathryn M. Jones

Employment History

Scientist, EAWAG *2025 – present | Dave Johnson | Dübendorf, CH*

- Researching sequences that cause ribosomal pausing in diverse bacteria using ribosomal profiling data

Postdoctoral researcher, LMU Munich *2023 – 2025 | Jürgen Lassak | Munich, DE*

- Conceived and led a large collaborative project that studied off target post-translational modifications*
- Contributed to developing a FACS-based fluorescent reporter to quantify ribosomal stalling*
- Co-organized and ran an R workshop explicitly for experimental microbiologists*

Postdoctoral researcher, University of Zurich *2019 – 2023 | Andreas Wagner | Zurich, CH*

- Conceived and led a project tying genomic patterns to maximum growth rates across the bacterial tree of life*
- Conceived and led a project which identified complications arising from HGT in diverse bacterial lineages*

Visiting Ph.D. student, Institut Pasteur *2018 | Eduardo Rocha | Paris, FR*

- Conceived and led a collaborative project to detect unlinked rRNA genes (non-operonic 16S and 23S) in environmental samples using long read sequencing through the Chateaubriand Fellowship*

Ph.D. student, University of Colorado Boulder *2014 – 2019 | Noah Fierer | Boulder, CO, USA*

- Assembled genomes from metagenomic data to characterize poorly studied deep-soil microbial communities*
- Contributed to developing a 'global atlas' of the 500 most abundant soil bacterial species, categorized these species into distinct ecological clusters and predicted their distribution worldwide*
- Led the analysis of one of the first metagenome-assembled genomes of an uncultivated soil bacterium*

* *contain links to relevant publications*