

Resource Summary Report

Generated by [dkNET](#) on Sep 17, 2026

Microbial eukaryotic 18S tag-sequence processing/QC - V4 region (automating)

DOI:10.17504/protocols.io.j9bcr2n

Type: Protocol

Proper Citation

Sarah Hu 2017. Microbial eukaryotic 18S tag-sequence processing/QC - V4 region (automating). protocols.io [dx.doi.org/10.17504/protocols.io.j9bcr2n](https://doi.org/10.17504/protocols.io.j9bcr2n)

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.j9bcr2n>

Authors: Sarah Hu

Group: Caron Lab - Protistan Ecology

Summary: This protocol provides step-by-step instructions for implementing a perl script to easily automate quality checking of raw tag sequences. This was specifically constructed for the numerous 18S diversity projects (which target the V4 hypervariable specific for evaluating protistan diversity). It is highly recommended that you follow along this Github repo: https://github.com/shu251/QC_steps_V4_tagsequencing

Affiliations: University of Southern California

External URL: https://github.com/shu251/QC_steps_V4_tagsequencing

Version: 2

Publication Date: 2017

Proper Citation: Sarah Hu 2017. Microbial eukaryotic 18S tag-sequence processing/QC - V4 region (automating). protocols.io [dx.doi.org/10.17504/protocols.io.j9bcr2n](https://doi.org/10.17504/protocols.io.j9bcr2n)

Record Creation Time: 20210329T220523+0000

Record Last Update: 20210329T220901+0000

Data and Source Information

Source: