

Resource Summary Report

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Using De-MetaST-BLAST

DOI:10.17504/protocols.io.ii2ccge

Type: Protocol

Proper Citation

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.ii2ccge>

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Group: The Aquatic Microbial Ecology Research Group - AMERG (The Buchan, Zinser and Wilhelm labs), Samantha R Coy's Protocols

Summary: Please contact Dr. Steven Wilhelm (wilhelm@utk.edu) or Samantha Coy (srose16@utk.edu) for additional information regarding this protocol. De-MetaST-BLAST, written in C++, is a script that can validate degenerate primers by performing in silico PCR amplification of the primers against metagenomic and metatranscriptomic databases (e.g. CAMERA; MG-RAST). The output is a list of in-silico PCR amplicons that are then blasted against GenBank to determine the most homologous sequence to the amplicon. Modified from Gulvik, C. A., Effler, T. C., Wilhelm, S. W., & Buchan, A. (2012). De-MetaST-BLAST: A Tool for the Validation of Degenerate Primer Sets and Data Mining of Publicly Available Metagenomes. PLoS ONE,7(11). doi:10.1371/journal.pone.0050362

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