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## Environmental DNA Metabarcoding- Full Pipeline Collection

DOI

[dx.doi.org/10.17504/protocols.io.eq2lywxwpvx9/v1](https://dx.doi.org/10.17504/protocols.io.eq2lywxwpvx9/v1)

Hakai

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Hakai Genomics



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**Protocol status:** Working

**We use this collection and it's working**

**Created:** June 19, 2024

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**Collection Integer ID:** 102123



## Abstract

This is a collection of protocols used to analyze environmental DNA (eDNA) of seawater samples.

As part of the Hakai Institute Ocean Observing Program, biomolecular samples have been collected weekly from 0 m to near bottom (260 m), to genetically characterize plankton communities in the Northern Salish Sea since 2015. These protocols are developed to work across all domains of life, from viruses to prokaryotes to eukaryotes, allowing for both amplicon sequencing and shotgun sequencing.

***This pipeline includes the following steps:***

**1. Seawater filtration:** Our standard protocol for filtering seawater on sterivex filters. Alternatives may be used.

**2. DNA extraction from sterivex filters:** Here we offer two alternatives:

- The robust Phenol Chloroform extraction protocol is used in our long-term monitoring program.
- A kit alternative requires less handling of toxic chemicals, and are used for stand-alone projects.

**3. DNA metabarcoding, library prep, and sequencing:** With the options of analyzing different marker genes:

- 18S rRNA nuclear gene: Diversity of Eukaryotes. (Balzano et al 2015)
- COI mitochondrial gene: Diversity of marine invertebrates. (Leray et al 2013)
- 12S rRNA mitochondrial gene: Diversity of fish. (Miya et al 2015)

## **4. Bioinformatic analyses**

Examples bioinformatic analysis for the different genes can be found on our GitHub page:

<https://github.com/hakaigenomics>

*More information to be found under each protocol:*



## Files

## Protocol



NAME

Seawater Filtration for Microbial or Environmental DNA

VERSION 1

CREATED BY

**Andreas Novotny**  
University of British Columbia[OPEN](#) →

## Protocol



NAME

DNA Extraction from 0.22µm Sterivex Filters - Phenol-Chloroform

VERSION 1

CREATED BY

**Andreas Novotny**  
University of British Columbia[OPEN](#) →

## Protocol



NAME

DNA Extraction from 0.22µm Sterivex Filters - Qiagen Blood and Tissue Kit

VERSION 1

CREATED BY

**Andreas Novotny**  
University of British Columbia[OPEN](#) →

## Protocol



NAME

18S rRNA-Gene Metabarcoding Library Prep: Dual-PCR Method

VERSION 1

CREATED BY



**Andreas Novotny**  
University of British Columbia

**OPEN** →

## Protocol



NAME

**COI-Gene Metabarcoding Library Prep: Dual-PCR Method**

**VERSION 1**

CREATED BY



**Andreas Novotny**  
University of British Columbia

**OPEN** →

## Protocol



NAME

**12S rRNA-Gene Metabarcoding Library Prep: Dual-PCR Method**

**VERSION 1**

CREATED BY



**Andreas Novotny**  
University of British Columbia

**OPEN** →