

Resource Summary Report

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Preparing biological samples for metabarcoding

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Type: Protocol

Proper Citation

Tim Regan 2020. Preparing biological samples for metabarcoding. protocols.io
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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.bms8k6hw>

Authors: Tim Regan

Summary: This protocol describes the preparation of biological samples (specifically from a marine environment e.g. hatchery or RAS unit) for amplicon sequencing. Starting with a biological sample stored in Qiagen buffer ATL, or similar, it begins with a bead beating process to homogenise the sample. Enzymatic lysis using Metapolyzyme and Proteinase K are employed to ensure efficient DNA release. The Qiagen DNeasy kit is used to column extract DNA from lysates. Following concentration estimates of DNA elutions, samples are diluted >1:10 to avoid PCR inhibition during amplicon library preparation.

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