



Version 2

Sep 28, 2020

# Preparing biological samples for metabarcoding V.2

Tim Regan<sup>1</sup><sup>1</sup>The Roslin Institute, University of Edinburgh

1

Works for me

[dx.doi.org/10.17504/protocols.io.bms8k6hw](https://dx.doi.org/10.17504/protocols.io.bms8k6hw)

Tim Regan

## ABSTRACT

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.

## DOI

[dx.doi.org/10.17504/protocols.io.bms8k6hw](https://dx.doi.org/10.17504/protocols.io.bms8k6hw)

## PROTOCOL CITATION

Tim Regan 2020. Preparing biological samples for metabarcoding. **protocols.io**<https://dx.doi.org/10.17504/protocols.io.bms8k6hw>

Version created by Tim Regan

## KEYWORDS

Metabarcoding, metagenomics, DNA extraction

## LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

## CREATED

Sep 28, 2020

## LAST MODIFIED

Sep 28, 2020

## PROTOCOL INTEGER ID

42560

## GUIDELINES

In every step following enzymatic digestion of samples (and in general), ensure samples are kept at 4C to maximise sample stability.

Freeze DNA samples if not being used for >1 week following extraction.

Otherwise, storing DNA at 4C in fridge is preferable.

## MATERIALS

NAME	CATALOG #	VENDOR
<a href="#">Buffer AL</a>	19075	
<a href="#">QIAgen DNeasy Blood and Tissue Kit, 50 rxn</a>	69504	<a href="#">Qiagen</a>
<a href="#">Buffer ATL</a>	19076	<a href="#">Qiagen</a>
<a href="#">Proteinase K, 100mg</a>	V3021	<a href="#">Promega</a>

NAME	CATALOG #	VENDOR
PBS		
Ethanol 70%		
MetaPolyzyme	MAC4L-5MG	Sigma Aldrich
UltraPure <sup>®</sup> ; DNase/RNase-Free Distilled Water	10977015	Thermo Fisher
Lysing Matrix A 2 mL tube	SKU 116910050-CF	MP Biomedicals

#### STEPS MATERIALS

NAME	CATALOG #	VENDOR
Buffer ATL	19076	Qiagen
Lysing Matrix A 2 mL tube	SKU 116910050-CF	MP Biomedicals
MetaPolyzyme	MAC4L-5MG	Sigma Aldrich
Proteinase K, 100mg	V3021	Promega
Buffer AL, Lysis buffer	19076	Qiagen
QIAgen DNeasy Blood and Tissue Kit, 50 rxn	69504	Qiagen

#### MATERIALS TEXT

Centrifuge.  
Bead beater.  
Incubator (for 37C and 56C).  
Pipettes and tips.

#### SAFETY WARNINGS

Refer to manufacturer's MSDS information for each reagent used to ensure appropriate and safe use.

#### DISCLAIMER:

##### DISCLAIMER – FOR INFORMATIONAL PURPOSES ONLY; USE AT YOUR OWN RISK

The protocol content here is for informational purposes only and does not constitute legal, medical, clinical, or safety advice, or otherwise; content added to [protocols.io](https://protocols.io) is not peer reviewed and may not have undergone a formal approval of any kind. Information presented in this protocol should not substitute for independent professional judgment, advice, diagnosis, or treatment. Any action you take or refrain from taking using or relying upon the information presented here is strictly at your own risk. You agree that neither the Company nor any of the authors, contributors, administrators, or anyone else associated with [protocols.io](https://protocols.io), can be held responsible for your use of the information contained in or linked to this protocol or any of our Sites/Apps and Services.

#### ABSTRACT

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.

#### BEFORE STARTING

Ensure leaving time for samples to thaw if frozen. Avoid leaving samples thaw for too long as this may lead to degradation.

#### Bead beating 45m

- Starting with biological sample (filter, swab, water, biofilm, tissue etc.) stored in Qiagen Buffer ATL (or similar), transfer up to <sup>30m</sup> 1 mL to Matrix A bead tube.



### Buffer ATL

by Qiagen

Catalog #: 19076



### Lysing Matrix A 2 mL tube

by MP Biomedicals

Catalog #: SKU 116910050-CF

- 2 Perform bead beating in a disruptor at at 5.0 M/s (speed) for 00:00:40 x2 (ensure tube looks somewhat homogenous). 15m

## Enzymatic digestion

2h 15m

- 3 Add 5  $\mu$ l of Metapolyzyme to each tube and vortex briefly. 2h 15m  
Incubate samples at 37 °C for 02:00:00 .



### MetaPolyzyme

by Sigma Aldrich

Catalog #: MAC4L-5MG

- 4 Add 20  $\mu$ l of Proteinase K to each tube, vortex for 00:00:10 , then incubate at 56 °C Overnight . 16h



### Proteinase K, 100mg

by Promega

Catalog #: V3021

## DNA extraction

- 5 Vortex samples for 00:00:15 and centrifuge a 13000 x g for 00:01:00 .
- 6 Transfer the supernatant from each tube (up to 900  $\mu$ l ) into a new tube and centrifuged at

🌀 **13000 x g, 00:01:00** .

- 7 Transfer up to **600 µl** of bead-free supernatant to a new **2 mL** tube.
- 8 Premix 70% ethanol and Qiagen lysis buffer AL 1:1 to add to sample at a ratio of 1:1:1  
e.g. for 10 samples of **500 µl** each, premix **550 µl** of buffer AL and **550 µl** of 70% ethanol and add **1 mL** of ethanol/buffer AL mixture to each sample.



Buffer AL, Lysis buffer

by Qiagen

Catalog #: 19076

- 9 Hereafter, the manufacturer's protocol for the Qiagen DNeasy Blood and Tissue kit is followed with some modifications:
  - Load < **600 µl** of lysate mixture (ATL, AL and EtOH) at a time into the column
  - Spin at **6000 x g, 00:01:00** and discard flow-through.
  - Repeat as necessary until all lysate is loaded on column e.g. mixture of **1500 µl** may take x3 initial spins and flow through discarding to complete column binding.



QIAGEN DNeasy Blood and Tissue Kit,  
50 rxn

by Qiagen

Catalog #: 69504

- 10
  - Place the DNeasy Mini spin column in a new **2 mL** collection tube (provided), add **500 µl** Buffer AW1, and centrifuge at **6000 x g, 00:01:00** (8000 rpm).
  - Discard flow-through and collection tube.
- 11
  - Place the DNeasy Mini spin column in a new **2 mL** collection tube (provided), add **500 µl** Buffer AW2, and centrifuge for at **20000 x g, 00:03:00** to dry the DNeasy membrane.
  - Discard flow-through and collection tube.
- 12 Perform final elution in **100 µl** of AE buffer.

#### Preparing concentration for library preparation

- 13 Check approximate concentration of extracted DNA using a Nanodrop.

- 14 Prepare 1:10 dilution of each extraction for PCR (to avoid PCR inhibition).  
Perform further dilution of sample to a maximum final concentration of ~  $[M]1 \text{ ng}/\mu\text{l}$  -  $[M]10 \text{ ng}/\mu\text{l}$
- 15 Use ~  $50 \text{ ng}$  of DNA in a  $20 \mu\text{l}$  per sequencing library PCR reaction (see amplicon library PCR protocol).