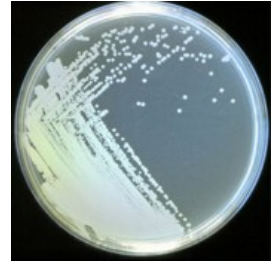


Jun 12, 2020

## Long-read DNA preparation for bacterial isolates.

DOI

[dx.doi.org/10.17504/protocols.io.64ghgtw](https://dx.doi.org/10.17504/protocols.io.64ghgtw)



He Sun<sup>1</sup>, Christian Brandt<sup>1</sup>, Anna Schnürer<sup>1</sup>

<sup>1</sup>Swedish University of Agricultural Sciences, Department of Molecular Sciences



He Sun

OPEN  ACCESS



DOI: [dx.doi.org/10.17504/protocols.io.64ghgtw](https://dx.doi.org/10.17504/protocols.io.64ghgtw)

**Protocol Citation:** He Sun, Christian Brandt, Anna Schnürer 2020. Long-read DNA preparation for bacterial isolates.. protocols.io <https://dx.doi.org/10.17504/protocols.io.64ghgtw>

**License:** This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

**Protocol status:** Working

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

**Created:** September 04, 2019

**Last Modified:** June 12, 2020

**Protocol Integer ID:** 27496

**Keywords:** bacterial isolate, Long-read DNA,



## Abstract

### General:

This is an optimized DNA isolation protocol adapted to the properties of bacteria isolated from biogas substrate and digestate, using NucleoBond® AXG Columns and NucleoBond® Buffer Set. The protocol reliably retrieves DNA of sufficient quality, length and yield. The performance has been validated on seven bacterial isolates from one biogas reactor and one biogas plant. Buffers and proteinase K can be found in NucleoBond Buffer Set III.

### Observed Performance on seven isolates runs using this protocol:

N50 Ranges between 22,000 and 46,000 bp. General throughput is between 16-22 Gigabases of a single flowcell (flowcell 106 Rev D, using the LSK-109 Kit).

### Funding:

This work was funded by the China Scholarship Council (CSC) [Grant No. 201606350190] and SLU.

## Materials

### MATERIALS

⊗ Agencourt AMPure XP **Beckman Coulter Catalog #A63880**




⊗ Ethanol

⊗ Lysozyme **Merck MilliporeSigma (Sigma-Aldrich) Catalog #L6876**










⊗ NucleoBond AXG 20 Columns **Macharey Nagal Catalog #740544**

⊗ NucleoBond Buffer Set III **Macharey Nagal Catalog #740603**

## Samples preparation

- 1 Add cation-adjusted Müller-Hinton broth in a 15 ml Falcon tube. (Müller-Hinton medium is used here for antibiotic-resistant bacteria)  
 5 mL CAMHB
- 2 Add 1/4 10 µl-loop of colony from an agar plate in the solution.
- 3 Vortex the mixture for 5 s at maximum speed.
- 4 Incubate the mixture overnight on a shaking bench at the speed of 120 rpm at 37 °C.  
 120 rpm  37 °C

## Cell disruption

- 5 Add 2 ml of the incubated mixture in a 2.5 ml Eppendorf tube.
- 6 Centrifuge the mixture.  
 5000 x g  20 °C  00:10:00
- 7 Discard the supernatant. (For anaerobes, due to low concentration of bacterial culture, it is suggested to repeat step 5 to step 7 several times in order to obtain enough amount of DNA)
- 8 Resuspend the bacterial pellet in Buffer G3 by vortexing.  
 1 mL Buffer G3
- 9 Add lysozyme and Proteinase K  
 20 µL lysozyme (100 mg/ml)  25 µL Proteinase K
- 10 Gently resuspend the mixture and incubate at 37 °C for 20 min without shaking.  
 37 °C  00:20:00
- 11 Add Buffer G4  
 400 µL Buffer G4



12 Gently resuspend the mixture and incubate at 50 °C for 30 min without shaking.



50 °C



00:30:00

13 Centrifuge the mixture.



5000 x g



20 °C



00:05:00

14 Transfer the supernatant to a 5 ml Eppendorf tube.

## Equilibration

15 Equilibrate the column (AXG 20) with Buffer N2.



1 mL Buffer N2

## Binding

16 Add Buffer N2 (room temperature) to the sample. Vortex the mixture for 15 s at maximum speed.



1 mL Buffer N2

17 Load 1 ml of the mixture on the column. Allow it to enter the resin by gravity flow.

18 Reload 1 ml of the mixture on the column. **Do not** reload if the mixture of former step has not been filtered completely in case the column gets clogged.

19 Reload the rest mixture.

## Wash

20 Wash the column with Buffer N3.




1 mL Buffer N3 three times

## Elution




- 21 Elute the genomic DNA with Buffer N5. Collect the DNA solution in a 2.5 ml Eppendorf tube.

 1 mL Buffer N5


#### Note

The average concentration of DNA is approximately 10 µg/ml.  
Store at 4 °C if you want to stop here

 4 °C Do not freeze


## Cleaning & condensing


- 22 Add magnetic Beads ( 0.35 volume, AMPure) to the DNA sample. Gently resuspend by hand.

 350 µL Magnetic beads

 1000 µL DNA sample

- 23 Incubate the mixture.

 00:10:00

 20 °C Room temperature

- 24 Spin down and let the beads bind to magnetic plate until the liquid is clear.

- 25 Stay on the magnet and remove supernatant.

- 26 Wash with Ethanol. Do not disturb pellet.

 150 µL Ethanol (80%)

- 27 Remove supernatant.

- 28  [go to step #26](#) Redo the washing once




29 Spin down and let the beads bind to magnetic plate again.  
Remove the residual liquid with a 10 µl pipette.

30 Add nuclease free water and resuspend gently.

 55 µL Nuclease free water

31 Incubate the DNA solution.

 00:15:00

 37 °C

32 Spin down and put on the magnetic plate.  
Retrieve the supernatant (DNA) with a 10 µl pipette.

#### Note

Determine dsDNA concentration e.g. by Qubit.  
Determine DNA length by Agarose gel or Bioanalyzer.